

Access DB# 63500

# SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval  
Reference Librarian  
Biotechnology & Chemical Library  
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## STAFF USE ONLY

Searcher: Jan  
Searcher Phone #: 4498  
Searcher Location: \_\_\_\_\_  
Date Searcher Picked Up: 4/1/02  
Date Completed: 4/1/02  
Searcher Prep & Review Time: \_\_\_\_\_  
Clerical Prep Time: 10  
Online Time: 10

### Type of Search

NA Sequence (#) \_\_\_\_\_  
AA Sequence (#) ✓  
Structure (#) \_\_\_\_\_  
Bibliographic \_\_\_\_\_  
Litigation \_\_\_\_\_  
Fulltext \_\_\_\_\_  
Patent Family \_\_\_\_\_  
Other \_\_\_\_\_

### Vendors and cost where applicable

STN \_\_\_\_\_  
Dialog \_\_\_\_\_  
Questel/Orbit \_\_\_\_\_  
Dr.Link \_\_\_\_\_  
Lexis/Nexis \_\_\_\_\_  
Sequence Systems ✓  
WWW/Internet \_\_\_\_\_  
Other (specify) \_\_\_\_\_



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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 68.03 Seconds

(without alignments)  
263.134 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MTVLAPAMSPPTLYLLLLLL.....RPGEQVPVPSPQDLLVH 235

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_68:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	138440	flt3 ligand - huma
2	864.5	69.6	245	S43293	FLT3/FLK2 ligand (
3	834	67.1	178	I39076	Flt3 ligand altera
4	768.5	61.9	231	A49265	FLT3/Flk-2 ligand
5	606.5	48.8	220	S43291	FLT3/FLK2 ligand (
6	606.5	48.8	220	I58343	flt3 ligand isofo
7	93	7.5	1217	T22672	hypothetical prote
8	92	7.4	661	TNBE12	74k alpha trans-in
9	89.5	7.2	474	I19543	hypothetical prote
10	89	7.2	387	I48201	adhalin - golden h
11	88.5	7.1	793	S60735	splicing factor SF
12	88.5	7.1	1386	T00257	hypothetical prote
13	88	7.1	753	J00532	OP protein - kenne
14	87.5	7.0	479	A32290	protein-tyrosine-p
15	87	7.0	910	A53137	tyrosine kinase re
16	86.5	6.9	590	A40437	glutamic acid-rich
17	86	6.9	299	T17832	hypothetical prote
18	86	6.9	485	A33647	sulfated surface g
19	86	6.9	746	T28004	hypothetical prote
20	85	6.8	366	A57374	Fc gamma (19c) rec
21	84	6.8	263	T03162	tegment protein 6
22	83.5	6.7	199	A39283	gamma-glutamyl car
23	83.5	6.7	199	E75630	hypothetical prote
24	83.5	6.7	530	A45690	transactivator EBN
25	83	6.7	1509	T19486	hypothetical prote
26	82.5	6.6	418	T19800	hypothetical prote
27	82.5	6.6	426	I36948	Ig epsilon-chain -
28	82.5	6.6	512	D40829	activin receptor 1
29	82.5	6.6	513	J01484	activin receptor p

30	82	6.6	106	2	T06479	proline/leucine-rl
31	82	6.6	854	2	T23837	hypothetical prote
32	81.5	6.6	485	2	C75460	hypothetical prote
33	81.5	6.6	488	2	S13423	stromelysin 3 (EC
34	81.5	6.6	958	2	T13593	hypothetical prote
35	81.5	6.6	1119	2	T50995	related to cytoske
36	81	6.5	196	2	B48232	cysteine-rich exte
37	81	6.5	209	2	A48232	cysteine-rich exte
38	81	6.5	388	2	S15591	probable transpos
39	81	6.5	428	1	EHU4	Ig epsilon chain C
40	80.5	6.5	636	2	JW0047	class I cytol kinase
41	80.5	6.5	1176	2	T49482	hypothetical prote
42	80.5	6.5	1306	2	T13592	hypothetical prote
43	80.5	6.5	1402	2	I46707	translation initia
44	80	6.4	398	2	T52311	isopenicillin N ep
45	80	6.4	434	2	S74706	(S)-2-hydroxy-acid

## ALIGNMENTS

```
RESULT 1
138440
flt3 ligand - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 01-Dec-2000
C:Accession: I38440; I39075; S43292
R:Lyman, S.D.; James, L.; Johnson, L.; Brasel, K.; de Vries, P.; Escobar, S.S.; Downe
Blood 83, 2795-2801, 1994
A>Title: Cloning of the human homologue of the murine flt3 ligand: a growth factor fo
A:Reference number: I38440; MUID:94235842
A:Accession: I38440
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U03858; NID:9494978; PIDN:AAA19825.1; PID:9494979
R:Lyman, S.D.; Stocking, K.; Davidson, B.; Fletcher, F.; Johnson, L.; Escobar, S.
Oncogene 11, 1165-1172, 1995
A>Title: Structural analysis of human and murine flt3 ligand genomic loci.
A:Reference number: I39075; MUID:96032581
A:Accession: I39075
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: EMBL:U29874; NID:91072036; PIDN:AAA90949.1; PID:91072037
R:Hannum, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zuzawski, S.; Bazan, J.F.;
Felt, A.; Menich, M.; Kelnier, G.; Namioka, M.G.; Renwick, D.; Roncarolo, M.G.; Zlotnik
Nature 368, 643-648, 1994
A>Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopo
A:Reference number: S43290; MUID:94195428
A:Accession: S43292
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-71, 'A', '73-235 <HAN>
A:Cross-references: GB:U04806; NID:9483844; PIDN:AAA17999.1; PID:9483845
C:Genetics:
A:Note: the authors translated the codon AGT for residue 25 as Met
A:Introns: 11/3; 48/3; 66/3; 114/3; 161/1; 220/3

Query Match 100.0%; Score 1242; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.8e-99;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTLYLLLLSSGLSGTDCSPQHSPISSDPAVKIIRLSDYLLADYPTV 60
DB 1 MTVLAPAMSPPTLYLLLLSSGLSGTDCSPQHSPISSDPAVKIIRLSDYLLADYPTV 60
QY 61 ASNLDDEELCGGLRLVLQAORMERLKYAGSKMGLLERVNTETHPYTKCAFQPPPSCL 120
DB 61 ASNLDDEELCGGLRLVLQAORMERLKYAGSKMGLLERVNTETHPYTKCAFQPPPSCL 120
QY 121 RRVQINIRSLQETSEQLVALKFWITRONFSRCLDCCQPDSSTLPPMSPRLPLATVPT 180
```

D <sub>b</sub>	121	R	V	T	N	I	S	R	L	Q	E	T	S	E	G	A	L	K	P	M	T	T	Q	N	S	R	C	L	E	O	Q	P	R	S	S	T	L	P	P	N	S	P	R	L	E	A	A	P	T	180
Q <sub>y</sub>	181	A	P	O	P	L	L	L	L	L	P	G	L	L	L	L	L	A	A	M	C	L	H	M	O	R	T	R	R	R	P	R	G	E	O	V	P	P	S	P	O	D	L	L	V	E	H	235		
D <sub>b</sub>	181	A	P	O	P	L	L	L	L	L	P	G	L	L	L	L	L	L	A	A	M	C	L	H	M	O	R	T	R	R	R	P	R	G	E	O	V	P	P	S	P	O	D	L	L	V	E	H	235	

## RESULT 2

```

FLTT3/FLK2 ligand (clone S109) - human
C:Species: Homo sapiens (man)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43293

```

felt, A.; Muench M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A. Nature 368, 643-648, 1994

A:Title: Ligand for FLT3/FLT2 receptor tyrosine kinase regulates growth of haematopoietic

A:Reference number: S43250; MUID:94195428

Query Match	69.6%;	Score 864.5;	DB 2;	Length 245;
Best Local Similarity	73.0%;	Pred. No. 8.5e-67;		
Matches 176; Conservative	7;	Mismatches 27;	Indels 31;	Gaps 3;

QY 61 ASNIQDEELCGGLMRLVLAQRMRERLKTIVAGSKNQGLLEAVNTETLHFTKCAFQPPSC L 120

DB 61 ASNIQDEELCGGLMRLVLAQRMRERLKTIVAGSKNQGLLEAVNTETLHFTKCAFQPPSC L 120

```
QY      121 RFVQNISRLIQTSEGLVALKPWITRQNSRCLELQCQDDSTLPWPMSRPLEATAPT 1800
        ||||| | | | |
        ||||| : ||| |
        |||||
Db       121 RFVQNISRLIQTSEGLVALKPWITRQNSRCLELQCQPGA--PRQSGGPAACGALT 1777
```

```
Oy      181 A P O P ----- P L L L L L L P V G L L L A A M C L H M O T R R R R P E Q V P V P S P    227
          |         |         |         |         |         |         |         |         |         |
Db      178 W P R P R P G E D T E A N H R G S P ----- A R G C I A W I Q R K L A N G R S L P M A R L I P S P    222
```

### RESULT 3

Flt3 ligand alternatively spliced isoform - human

Flt3 ligand alternatively spliced isoform - human

C:\species: Homo sapiens (man)  
C:\date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C/cession: 1350/06  
Rlyman, S.D.; Stocking, K.; Davison, B.; Fletcher, F.; Johnson, L.; Escobar, S.  
Oncogene 11, 1165-1172, 1995

A:Accession: I39076  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

Query Match	67.1%	Score	834	DB 2:	length	178;
Best Local Similarity	100.0%	Pred. No.	2	de=64;		
Matches 160;	Conservative	0;	Mismatches	0;	Indels	0;
					Gaps	0;

[illegible]

Qy	121	RVQGTNISRLLOETSEQLVALKPWITRQNFSSRCLELQCP	160
Db	121	RVQGTNISRLLOETSEQLVALKPWITRQNFSSRCLELQCP	160

```
Qy 121 RFQVNTSRLLQETSEQLVAKKWITRQNFSCLELQCP 160
    |||||
Db 121 RFQVNTSRLLQETSEQLVAKKWITRQNFSCLELQCP 160
```

## RESULT 4

```

flt3/flk-2 ligand precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1995
C:Accession: A49265; I49347; I49346; S43290

```

RiLYman, S.D., James, L., Vanden Bos, T., de Vries, P., Brasel, K., Gliniak, B., Holl  
D.L., Williams, D.E.; Beckmann, M.P.  
Cell 75, 1157-1167, 1993  
A:Title: Molecular cloning of a ligand for the flt3/flk-2 tyrosine kinase receptor: a  
A:Reference number: A49265; MUID:94084791

A:Title: Structural analysis of human and murine flt3 ligand genomic loci.  
A:Reference number: 139075; MUID:96032581

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Accession: I49346  
A:Cross-references: EMBL:U029875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041  
A:Residues: 1-163; G, 165, 'HYAG' <RES>  
A:Credits-references: EMBL:U029875; NID:g1072039; PIDN:AAA90952.1; PID:g1072041

felt, A.; Muench, M.; Kellner, G.; Namikawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik  
 Nature 368, 643-648, 1994  
 A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic  
 A:Reference number: S43290; MUID:94195428  
 A:Accession: S43290

A:Experimental source: clone 1110  
A:Note: the sequence from Fig. 2c is inconsistent with that from Fig. 2a in having 4-  
C:Genetics:  
A:introns: 11/3; 49/3; 67/3; 115/3; 164/1; 224/3  
C:Keywords: transmembrane protein

	Matches 163;	Conservative 17;	Mismatches 43;	Indels 9;	Gaps
QY	1	MTVLPAWSP-ITYYLLLLSSGLSGQDCSFQSPISPSDAVKIRRLSYLLQDYVPT	59		
Db	1	MTVLPAWSPNSLSLLSSGLSGQDCSFQSPISPSDAVKIRRLSYLLQDYVPT	60		

Db 121 LRFVGTINSHLTKTCTGQLLAKRCICKACQNSRCLEVCQDPSSLTLPSPRSIALEAT 180

Qy 178 APTAQP - LLLDLLPVGILLAAACMLHMQTRRRTRPGEQVPPVSP 227

Db 181 ELPPRRQQLLLLLLPPLVLIVLAAAGLRMQARRK----GELHGVGLP 228

```

RESULT      5
S43291
FLT3/FLK2 ligand (clone T118) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S43291
R:Hannun, C.; Culpepper, J.; Campbell, D.; McClanahan, T.; Zurawski, S.; Bazan, J.F.; Kiehl, A.; Muench, M.; Keiner, G.; Nankawa, R.; Rennick, D.; Roncarolo, M.G.; Zlotnik, A.
Nature 368, 643-648, 1994
A:Title: Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of haematopoietic
A:Reference number: S43290; MUID:94195428
A:Accession: S43291
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-220 <HAN>

```

Query Match	48.8%	Score 606.5	DB 2	Length 220
Best Local Similarity	61.5%	Pred. No. 9.4e-45		
Matches 134	Conservative 18	Mismatches 43	Indels 23	Gaps 5

[illegible]

RESULT 6  
158343  
flt3 ligand isoform 5H - mouse  
C:Species: Mus sp. (mouse)  
C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: 158343  
R:Lyman, S.D.; James, L.; Escobar, S.; Downey, H.; de Vries, P.; Brasel, K.; Stocking, M.  
OncoGene 10, 149-157, 1995  
A:Title: Identification of soluble and membrane-bound isoforms of the murine flt3 ligand  
A:Reference number: 158343; MUID:95124710  
A:Accession: 158343  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-220 <RES>  
A:Cross-references: GB:S76459; NID:g913479; PIDN:AAB33069.1; PID:g913480

[illegible]

```

Db      61  VAVNLDDEKCKALMSLELAARMYLEOLKTVAAGSKMOTLLDEVTNEIFHVSCTFORLPBC 120
Oy      120  LRPVOTNSTRLEOISBGLVAKPMITR--ONFSRCLELOOPSSSLPRMSPRP--- 173
Db      121  LRFVQTNSHLLKDTCTCYLLAKKICIGKACONFSRCLEVCQOQONG-----GPRADHNG 174
Oy      174  ---LEATPAPARPLL-----LLLPVGLLLAA 201
Db      175  ATRLATALLTVCGGLLLPLVGTSHMFFLLPPLFSLSS 212

```

RESULT 7  
T22672  
hypothetical protein F54F12.1 - *Caenorhabditis elegans*  
C/Species: *Caenorhabditis elegans*  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C/Accession: T22672  
R:Barlow, K.  
submitted to the EMBL Data Library, November 1996  
A/Reference number: Z19597  
A/Accession: T22672  
A/Status: preliminary; translated from GR/EMBL/DBD  
A/Molecule type: DNA  
A/Residues: 1-1217 <MIL>  
A/Cross-references: EMBL:Z81548; NID:e1062020; PIDN:CB04464.1; GSPDB:GN00021; CESP:F54F12  
C/Genetics:  
A/Experimental source: clone F54F12  
A/Gene: CESP:F54F12.1  
A/Map position: 3  
A/Introns: 742/2; 826/1; 884/2; 922/3; 972/1; 1024/2; 1102/1

[illegible]

```

RESULT      8
TNBE12
74K alpha trans-inducing protein - human herpesvirus 3
C:Species: human herpesvirus 3, varicella-zoster virus
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
C:Accession: C27342
R:Davidson, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A:Title: The complete DNA sequence of varicella-zoster virus.
A:Reference number: A27345; MUID:86306657
A:Accession: C27342
A:Molecule type: DNA
A:Residues: 1-661 <DAV>
A:Cross-references: EMBL:X04370; NID:g59895; PIDN:CAA27895.1; PID:g60001
C:Genetics:
A:Gene: 12
C:Superfamily: herpesvirus 77K alpha trans-inducing protein
C:Keywords: trans-inducing protein; transcription regulation

```

Query Match	7.4%	Score	92	DB	1	Length	661
Best Local	Similarly	26.6%	Pred.	No.	3.8		
Matches	61	Conservative	29	Mismatches	103	Indels	36
						Gaps	11

QY 19 LLSGSGSGTODCS---FQHSPISSDPAVKI--RELSDYLLQDYPTVYASNLQDEELCG-71  
 A:Accession: I48201  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482  
 C:Superfamily: mouse adhalin

Db 79 LTPSPVLQSTERSHSLGLHNNNNPESLVSCMSNDVHDCFMQRYMETIQCLDLKLISGD 138  
 72 GWRRLVLAQRMERLKTIVASCKMGLLERN-----VEHFVTKCAQOP---PPSCIRFV 123  
 139 GLM-WYENTYTWOLKTYTGAEPVTVSEKYNKSKSTVLLFSSVYAKKPSIRPFKSKI 197  
 124 QTNISRLQETSEQLVALKPWITRQNFSCLELQCPDSSSTLPPMSP-RPLEATAPAP 182  
 198 NSDYRGICQELREALGAVQYK---YEMR-----PDDPTNPSPDIRINQELAAVTAT 247  
 QY 183 QPRLLLLLLPVGLLLIAAAMCHMORTRRTPRPGEQVPPVSPDGL 231  
 248 GYGMMFMFLDVPD-----ARVCRHLKLOFRIRIRGPRASV----IPDDL 287

## RESULT 9

hypothetical protein C28D4.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T19543  
 R:McMurray, A.  
 Submitted to the EMBL Data Library, November 1996  
 A:Reference number: Z19139  
 A:Accession: T19543  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-474 <MTL>  
 A:Cross-references: EMBL:282259; PIDN:CAB05129.1; GSPDB:GN00022; CESP:C28D4.2  
 A:Experimental source: Clone C28D4  
 C:Genetics:  
 A:Gene: CESP:C28D4.2  
 A:Map position: 4  
 A:Introns: 26/3; 72/3; 118/2; 169/1; 203/2; 240/2; 262/3; 298/3; 342/2; 391/3

Query Match 7.2%; Score 89.5; DB 2; Length 474;  
 Best Local Similarity 24.1%; Pred. No. 4.2;

Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;

QY 27 TQDC-----SFQHS-PISSDPAVKIREL-SYLLQDYPTVYASNLQDEELCGGLMRL 76  
 65 TTCCVDLKKVSKFSDSSAPISGELLFRARPLCAKYL-----GGAMRK 106  
 77 VLAQRMERLKTIVASCKMGLLERNVEHFVTKCAQOPPPSCLR-FVQTNISRLQET- 134  
 107 VKIEEF--RIRATIGG-MSNLLFLVELPAH-LTPIQMEPEKALLRVQCSDIDQLSESV 162  
 QY 135 -----SEQLVALKPWITRQNFSCLELQ-----QPDSSSTLPPMSPR-PLEATA 178  
 163 VFTLLSERNLGPKMLGVPGRGFEQFIPSRALQCLEISKPGLSKLIAPIVARVHTLDAP 222  
 QY 179 PTPAPQPLLLLPVGLLLIAAAMCHMORTRRTP---RPGF-----QVPPVSPD 229  
 223 PKPEQ-----TLQTAQRMERF---KKTAPAGERPIEMLYLQAKVPSDYPT 266  
 QY 230 LLVE 234  
 267 ITVAQ 271

## RESULT 10

adhalin - golden hamster  
 C:Species: Mesocricetus auratus (golden hamster)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 20-Jun-2000  
 C:Accession: I48201  
 R:Roberts, J. L.; Campbell, K. P.  
 FEBS Lett. 364, 245-249, 1995  
 A:Title: Adhalin mRNA and cDNA sequences are normal in the cardiomyopathic hamster.  
 A:Reference number: I48201; M0ID:95278335

A:Accession: I48201  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-387 <RES>  
 A:Cross-references: EMBL:U21677; NID:g726481; PIDN:AAA81645.1; PID:g726482  
 C:Superfamily: mouse adhalin

Query Match 7.2%; Score 89; DB 2; Length 387;  
 Best Local Similarity 23.4%; Pred. No. 3.7;

Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYLLLLLSGSGTODCSFQHSPISSDPAVKIRELSYLLQDYPTVYASNLQDEELC 70  
 115 TTRQRLLLI-----EDEGRPLPYQAEFLVRSHVEVL-----PSTPANRFL--TAL 161  
 QY 71 GGLMRL-----VLAQRMERLKTIVASCKMGLLERNVEHFVTKCAQOP-----K 110  
 162 GGLMELEQLDLNLTSLADRGKRVPLIEGRKGVYIKGSARPFSTCLKMVASPDSYAR 221  
 QY 111 CARQPP--SC-----LRFVQTNISRLQETSEQLVALKPWITRQNFSCLELQCPD 161  
 222 CAGQGPRLSLCYSGLAHPFVDMQNVSLVDKSVPEPLD-----EVPTPGD 266  
 QY 162 SSTLPPMSPRPLEAT-----APTAPQPLLLLPVGLLLIAAAMC----- 204  
 267 GLEHDPFCPPTEATGCRPLADALVTLVPLVALLL--TLLLAYIMCREGOLKRD 323  
 QY 205 -----LHMQRTPRRTPRP-----GEOVPP-VSPQ-DLL 231  
 324 MATSDIOMVHCHTTHGNTTELROMAAREVPRPLSTLPMENVATGERLPPRVSAQVPL 383  
 QY 232 LEVH 235  
 384 LDQH 387

## RESULT 11

splicing factor SF3a 120K chain - human  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 21-Jul-2000  
 C:Accession: S60735; S60733  
 R:Kraemer, A.; Mulhauser, F.; Wersig, C.; Groening, K.; Bibe, G.  
 RNA 1, 260-272, 1995  
 A:Title: Mammalian splicing factor SF3a120 represents a new member of the SUPR family  
 A:Reference number: S60733; M0ID:96079958  
 A:Accession: S60735  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: protein  
 A:Residues: 1-793 <KRA>  
 A:Cross-references: EMBL:X85237; NID:g899297; PIDN:CAA59494.1; PID:g899298  
 A:Accession: S60733  
 A:Molecule type: protein  
 A:Residues: 51-62; 82-94; 270-275; 397-414; 448-463 <KRA2>  
 C:Genetics:  
 A:Gene: GDB:SF3A120; PRP21; SAP114  
 A:Cross-references: GDB:9955873  
 A:Map position: 22q12.1-22qter  
 C:Superfamily: human splicing factor SF3a 120K chain; ubiquitin homology  
 C:Keywords: pre-mRNA splicing  
 F:714-790/Domain: ubiquitin homology <UBH>

Query Match 7.2%; Score 89; DB 1; Length 793;  
 Best Local Similarity 22.3%; Pred. No. 8.4;

Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPAWSPTTYLLLLLSGSGTODCSFQHSPISSDPAVKIRELSYLLQDYPTVYASN 63  
 401 LAPAPAPDEVLY-----SPITGE--KI-----PASK 424  
 Db 64 LDQELCGGLMRLVLAQRMERLKTIV-----AGSKMGLLERNVEHF 107

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Db 425 MOENHRIG-----LLDPRLWLEQDRSIREKQSDDEVYAPGLDIESLKLQALR-RTDIFG 478
QY 108 VTKCA-----FQPPPSCLRF-----VQTNISRLQETSEQLVALKPMI 145
Db 479 VEETAIKGIKEEETIOKEEKEVTDGHSNARTQQAQANIT--LQROIENIRKAKGLV 536
QY 146 -----TRONF--SRCLELOCOP-----DSSTLP-----PMKSPRLKAT-----APT 180
Db 537 PEDDTKEIGTSKRENEITQQPPPPSSATNIFSSAPITSVPRPPMPPTVTSANPV 596
QY 181 APORPLLLLLLPGVGLLLAAMCLMORTR-----RTRPRGEOVPP--VPS 227
Db 597 MRRPMSVVALRPGOSVIAIPMPITIHARINVPMPSPAPIMARRPPMIVPTAFVAP 656

```

```

RESULT 12
T00257
hypothetical protein KIAA0476 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00257
R:Seiki, N.; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.;
DNA Res. 4, 345-349, 1997
A:Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human
A:Reference number: 214085; MUID:98116662
A:Accession: T00257
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1386 <SEK>
A:Cross-references: EMBL:AB007945; NID:g3413913; PIDN:BAA32321.1; PID:g3413914
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0476

```

```

Query Match 7.1%; Score 88.5; DB 2; Length 1386;
Best Local Similarity 23.1%; Pred. No. 17;
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

```

```

QY 21 SSGLSGTODCSFQHSPISSDPAVKIRELSYLLDYPYTVASNLQDELC---GGLMKL 76
Db 1104 SAGASGSKDAPVGGP-----GPLYSDRLCLA--LDEPOLCNGHMGASRR 1148
QY 77 VLAQRMRLKTVAGSKMOGLLERVTEIHFTKCAFQPPSCARFQTNISRLQETSE 136
Db 1149 VESGMAVLSPLVLRKELESIVENGESEV-----LALPELSAHPITFNNLMTYQRL-- 1201
QY 137 QLVALKPMTIRQNSRCLQCO--PDSSTLPPPW--SPRPLEA-----TAPTAQPP 185
Db 1202 RLPSLPGLVLA-----CDGSHSQAPSPMLTPDPASVQVRLMDVLTDPDNSCP 1253
QY 186 LLLLLLLVGLLLAAMCLMORTRRRTPRPGEOVPPVPSQDILLVE 234
Db 1254 LYLVL-----WRIHSQ--IPQRVWVG-----VVPASLSTALLE 1284

```

```

RESULT 13
J00532
OP: protein - Kennedy's yellow mosaic virus
C:Species: Kennedy's yellow mosaic virus
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-May-1999
C:Accession: J00532
R:Ding, S.; Keese, P.; Gibbs, A.
J. Gen. Virol. 71, 925-931, 1990
A:Title: The nucleotide sequence of the genomic RNA of Kennedy's yellow mosaic tymovirus-
A:Reference number: J00532; MUID:90218040
A:Accession: J00532
A:Molecule type: mRNA
A:Residues: 1-753 <DIN>
A:Cross-references: GB:D00637; NID:g221966; PIDN:BAA00531.1; PID:d1000966; PID:g221970
A:Experimental source: Strain Jervis Bay isolate

```

```

Query Match 7.1%; Score 88; DB 2; Length 753;
Best Local Similarity 22.3%; Pred. No. 9.6;
Matches 41; Conservative 19; Mismatches 58; Indels 66; Gaps 7;

```

```

QY 100 RVNTEIHFTVCAEQPPSCARF-----VQTNIS-----RLQETSEQLVALKPMI 147
Db 420 RLSTQPPSSPQTSSPPRPRTDASGIQTLASPRSKRKESLPRNHQ-----PRSHK 475
QY 148 QNFSR-----CLELQCPDSSSTLPPWSPRLKATATAPORPLLLLLLP----- 193
Db 476 RNLRRHSALRLPLRPHRTKTPQHPAVPQ--TAGPFRPHPTKRIPLHPKSGERNHSP 533
QY 194 -----VGLLLAAMCLMORTRRRTPRPGEOVPPVPS 226
Db 534 PDVDFHDCQPSPTSHVYGYRRLLSGSISLPKILFW-----RRKSPNARHLRPPPP 586
QY 227 PQDL 230
Db 587 PRKL 590

```

```

RESULT 14
A32290
protein-tyrosine-phosphatase (EC 3.1.3.48) cdc25 homolog string - fruit fly (Drosophila
C:Species: Drosophila melanogaster
C:Date: 05-Oct-1989 #sequence_revision 25-Apr-1997 #text_change 11-Jun-1999
C:Accession: A32290; S12008
R:Edgar, B.A.; O'Farrell, P.H.
Cell 57, 177-187, 1989
A:Title: Genetic control of cell division patterns in the Drosophila embryo.
A:Reference number: A32290; MUID:89195217
A:Accession: A32290
A:Molecule type: mRNA
A:Residues: 1-479 <EDG>
A:Cross-references: GB:M24909; NID:g158507; PIDN:AAA28916.1; PID:g158508
R:Jimenez, J.; Alphey, L.; Nurse, P.; Glover, D.M.
EMBO J. 9, 3565-3571, 1990
A:Title: Complementation of fission yeast cdc2(+) and cdc25(+) mutants identifies c
A:Reference number: S12008; MUID:91006056
A:Accession: S12008
A:Molecule type: mRNA
A:Residues: 1-227, 'A', 229-479 <JIM>
A:Cross-references: EMBL:X57495; NID:g7706; PIDN:CAA40732.1; PID:g7707
C:Genetics:
A:Gene: Flybase:stg
A:Cross-references: Flybase:FBgn0003525
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to peptidyl-tyrosine
A:Pathway: Initiation of mitosis
A:Note: cdc25 activates the cdc2 protein kinase by dephosphorylating it
C:Superfamily: protein-tyrosine-phosphatase string; cdc25-type protein-tyrosine-phosp
C:Keywords: cell cycle control; mitosis; phosphoprotein; phosphoric monoester hydroly
F:252-456/Domain: cdc25-type protein-tyrosine-phosphatase homolog <PRP>
F:379/Active site: Cys (phosphocysteine intermediate) #status predicted
F:385/Binding site: substrate phosphate (Arg) #status predicted

```

```

Query Match 7.0%; Score 87.5; DB 1; Length 479;
Best Local Similarity 22.9%; Pred. No. 6.3;
Matches 56; Conservative 34; Mismatches 76; Indels 79; Gaps 14;
QY 1 MIVLAPAMSPPTIYLL-----LLSSGLSGTQCSFQHSPISSDPAVKIRELSYLLDQVP 57
Db 72 MGLSLPEGSPQRFQIVROPKILPAMGVSS-----DHTPARS-FRI-ENSLSS-----T 117
QY 58 VIVASNLQDEELCGGLMRLVLAQRMRLKTVAGSKMOGLLERVTEIHFTVTKCAFOPP 117
Db 118 CSMSSMODE-----YMLPFEMSQSO-----QTALGF-----P 146
QY 118 SCLRFVQTNISRLQETSEQLVALKP--WTRQNFSCRLEL--QCQPDSSSTLPPWSPRP 173
Db 147 SGLN-----SLISQIKIQAPAAKSPAGLSMRRPSVRLCLSMTESNTSTTTPPKTPE- 199

```





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:16:39 ; Search time 68.97 Seconds

(without alignments)  
124.927 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MVLAPAWSPFTYLLLL...RPGEQVPPVSPDLLVER 235

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 3664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 FLJ3L_HUMAN	P49771 homo sapien
2	768	61.8	232	1 FLJ3L_MOUSE	P49772 mus musculu
3	92	7.4	661	1 ARI2_VZVD	P09264 varicella-z
4	89.5	7.2	941	1 GBR2_HUMAN	O75899 homo sapien
5	89	7.2	387	1 SGCA_MESAV	O64255 mesocricetu
6	89	7.2	793	1 S3AL_HUMAN	O15459 homo sapien
7	87.5	7.0	415	1 TNRG_MOUSE	P50284 mus musculu
8	87.5	7.0	479	1 MPIP_DROME	P20483 drosophila
9	87	7.0	910	1 DDRL_RAT	O63474 rattus norv
10	87	7.0	911	1 DDRL_MOUSE	O03146 mus musculu
11	86.5	7.0	1394	1 CNG4_BOVIN	O28181 bos taurus
12	86	6.9	485	1 SSGP_VOLCA	P21997 volvox cart
13	85	6.8	282	1 ATRF5_HUMAN	O922d1 homo sapien
14	85	6.8	366	1 FCGN_RAT	P13599 rattus norv
15	84	6.8	582	1 MNT_HUMAN	O09583 homo sapien
16	84	6.8	732	1 YF48_HUMAN	O94844 homo sapien
17	83.5	6.7	671	1 VZG2_HUMAN	O94847 homo sapien
18	83	6.7	758	1 VKGC_HUMAN	O94847 homo sapien
19	81.5	6.6	488	1 MM1L_HUMAN	P38435 homo sapien
20	81.5	6.6	591	1 MNT_MOUSE	P24447 homo sapien
21	81.5	6.6	2124	1 Y192_HUMAN	O08789 mus musculu
22	81	6.5	283	1 ATRF5_MOUSE	O93074 homo sapien
23	81	6.5	387	1 SGCA_MOUSE	O70191 mus musculu
24	81	6.5	428	1 EPC_HUMAN	P01854 homo sapien
25	81	6.5	1248	1 DIAL_HUMAN	O60610 homo sapien
26	80.5	6.5	1402	1 IF4G_RABIT	P41110 oryctolagus
27	80	6.4	397	1 CEPD_STRCL	P18849 streptomyce
28	80	6.4	940	1 GBR2_RAT	O88871 rattus norv
29	80	6.4	1174	1 KPCL_COCH	O12632 cochliobolu
30	80	6.4	1794	1 YAV1_SCHPO	O10172 schizosacch
31	79	6.4	805	1 YG6_YEAST	P53086 saccharomyc
32	78.5	6.3	251	1 HXB4_HUMAN	P17483 homo sapien
33	78.5	6.3	382	1 AVRB_RAT	P38445 rattus norv

34	78.5	6.3	387	1 SGCA_RABIT	O28686 oryctolagus
35	78.5	6.3	913	1 DDRL_HUMAN	O08345 homo sapien
36	78.5	6.3	1180	1 ATR1_HUMAN	O94811 homo sapien
37	78	6.3	205	1 CYSR_SYNY3	O55854 synchocyst
38	78	6.3	566	1 TS13_MOUSE	O01753 mus musculu
39	77.5	6.2	1885	1 FAS2_CANAL	P43098 c fatty aci
40	77.5	6.2	2004	1 MOZ_HUMAN	O92794 homo sapien
41	77	6.2	195	1 CORA_HPBVF	P29178 hepatitis b
42	77	6.2	316	1 CONC_HUMAN	P49918 homo sapien
43	77	6.2	367	1 MRCG_HUMAN	P16926 escherichia
44	77	6.2	478	1 BM3B_HUMAN	P53107 homo sapien
45	77	6.2	742	1 PKWA_THECU	P49695 thermomonos

## ALIGNMENTS

```

RESULT 1
ID FLJ3L_HUMAN STANDARD: PRT: 235 AA.
AC P49771:
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, last sequence update)
DT 20-AUG-2001 (rel. 40, last annotation update)
DE SL CYTOKINE PRECURSOR (FMS-RELATED TYROSINE KINASE 3 LIGAND) (FLT3
DE LIGAND).
GN FLT3LG
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195428; PubMed=8145851;
RA Hannum C., Cuipepper J., Campbell D., McClanahan T., Zurawski S.,
RA Bazan J.F., Kastelein R., Hudak S., Wagner J., Matsen J., Loh J.,
RA Duda G., Martina N., Peterson D., Menon S., Shanafelt A.,
RA Muench M., Kelnner G., Rosner O., Dubreuil P., Birnbaum D., Lee F.;
RA Zlotnik A., Rosner O., Dubreuil P., Birnbaum D., Lee F.;
RT "Ligand for FLT3/FLK2 receptor tyrosine kinase regulates growth of
RT haematopoietic stem cells and is encoded by variant RNAs.";
RL Nature 368:643-648(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94235842; PubMed=8180375;
RA Lyman S.D., James L., Johnson L., Brasel K., de Vries P.,
RA Escobar S.S., Downey H., Spielt R.R., Beckmann M.P., McKenna H.J.;
RT "Cloning of the human homologue of the murine flt3 ligand: a growth
RT factor for early hematopoietic progenitor cells.";
RL Blood 83:2795-2801(1994).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=96032581; PubMed=7366977;
RA Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
RA Escobar S.;
RT "Structural analysis of human and murine flt3 ligand genomic loci.";
RL Oncogene 11:1165-1172(1995).
CC - FUNCTION: STIMULATES THE PROLIFERATION OF EARLY HEMATOPOIETIC
CC CELLS. SYNERGIZES WELL WITH A NUMBER OF OTHER COLONY STIMULATING
CC FACTORS AND INTERLEUKINS.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. A SOLUBLE FORM
CC IS ALSO PRODUCED BY ALTERNATIVE SPLICING.
CC - ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -----
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RT \*Identification of a GABAB receptor subunit, gb2, required for functional GABAB receptor activity.\*  
 RT J. Biol. Chem. 274:7607-7610(1999).  
 RN [8]  
 RP R1A-R2 INTERACTION.  
 RX MEDLINE=2023752; PubMed=10773016;  
 RA Sullivan R., Chateaufort A., Coulombe N., Kolkowski L.F. Jr.,  
 RA Johnson M.P., Hebert T.E., Ethier N., Bellef M., Metters K.,  
 RA Abramovitz M., O'Neill G.P., Ng G.Y.K.;  
 RT "Coexpression of full-length gamma-aminobutyric acid(B) (GABA(B))  
 RT receptors with truncated receptors and metabotropic glutamate  
 RT receptor 4 supports the GABA(B) heterodimer as the functional  
 RT receptor." Exp. Ther. 293:460-467(2000).  
 RL J. Pharmacol. RECEPTOR FOR GABA. THE ACTIVITY OF THIS RECEPTOR IS  
 CC MEDIATED BY G-PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY,  
 CC STIMULATES PHOSPHOLIPASE A2, ACTIVATES POTASSIUM CHANNELS,  
 CC INACTIVATES VOLTAGE-DEPENDENT CALCIUM-CHANNELS AND MODULATES  
 CC INOSITOL PHOSPHOLIPIDS HYDROLYSIS. PLAYS A CRITICAL ROLE IN THE  
 CC FINE-TUNING OF INHIBITORY SYNAPTIC TRANSMISSION. PRE-SYNAPTIC  
 CC GABA-B-R INHIBIT NEUROTRANSMITTER RELEASE BY DOWN-REGULATING  
 CC HIGH-VOLTAGE ACTIVATED CALCIUM CHANNELS, WHEREAS POSTSYNAPTIC  
 CC GABA-B-R DECREASES NEURONAL EXCITABILITY BY ACTIVATING A PROMINENT  
 CC INWARDLY RECTIFYING POTASSIUM (KIR) CONDUCTANCE THAT UNDERLIES THE  
 CC LATE INHIBITORY POSTSYNAPTIC POTENTIALS. NOT ONLY IMPLICATED IN  
 CC SYNAPTIC INHIBITION BUT ALSO IN HIPPOCAMPAL LONG-TERM  
 CC POTENTIATION, SLOW WAVE SLEEP, MUSCLE RELAXATION AND  
 CC ANTIHYPOTENSION.  
 CC -1- SUBUNIT: HETERODIMER OF GABA-B-R1 AND GABA-B-R2. NEITHER OF WHICH  
 CC IS EFFECTIVE ON ITS OWN AND HOMODIMERIC ASSEMBLY DOES NOT SEEM TO  
 CC HAPPEN.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MOREOVER  
 CC COEXPRESSION OF GABA-B-R1 AND GABA-B-R2 APPEARS TO BE A  
 CC PERQUISITE FOR MATURATION AND TRANSPORT OF GABA-B-R1 TO THE  
 CC PLASMA MEMBRANE.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 2A (SHOWN HERE), 2B AND 2C; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN, ESPECIALLY IN  
 CC CEREBRAL CORTEX, THALAMUS, HIPPOCAMPUS, FRONTAL, OCCIPITAL AND  
 CC TEMPORAL LOBE, OCCIPITAL POLE AND CEREBELLUM, FOLLOWED BY CORPUS  
 CC CALLOSUM, CAUDATE NUCLEUS, SPINAL CORD, AMYGDALA AND MEDULLA.  
 CC WEAKLY EXPRESSED IN HEART, TESTIS AND SKELETAL MUSCLE.  
 CC -1- DOMAIN: ALPHA-HELICAL PARTS OF THE C-TERMINAL INTRACELLULAR REGION  
 CC MEDIATE HETERODIMERIC INTERACTION WITH GABA-B RECEPTOR 1.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.  
 CC GABA-B RECEPTOR SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: AJ012188; CA009942.1; -  
 DR EMBL: AF056085; AAC63228.1; -  
 DR EMBL: AF056723; AAC63383.1; -  
 DR EMBL: AF095724; AAC63384.1; -  
 DR EMBL: AF095784; AAC30389.1; -  
 DR EMBL: AF074483; AAD03336.1; -  
 DR EMBL: AF069755; AAC399345.1; -  
 DR EMBL: AF099033; AAD45867.1; -  
 DR InterPro: IPR001828; ANF\_receptor.  
 DR InterPro: IPR000337; GPCR\_Mgr.  
 DR Pfam: PF00003; 7tm\_3; 1.  
 DR Pfam: PF01094; ANF\_receptor; 1.  
 DR PRINTS: PR00248; GPCRMR.  
 DR PRINTS: PR01176; GABABRECEPTR.  
 DR PRINTS: PR01177; GABAB1RECEPTR.  
 DR PRINTS: PR01178; GABAB2RECEPTR.  
 DR PROSITE: PS50099; PRO\_RICH; 1.  
 DR PROSITE: PS00979; G\_PROTEIN\_RECCEP\_F3\_1; FALSE\_NEG.

DR PROSITE: PS00980; G\_PROTEIN\_RECCEP\_F3\_2; FALSE\_NEG.  
 DR PROSITE: PS00981; G\_PROTEIN\_RECCEP\_F3\_3; FALSE\_NEG.  
 DR PROSITE: PS50259; G\_PROTEIN\_RECCEP\_F3\_4; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Signal;  
 KW postsynaptic membrane; Colled coll; Alternative splicing;  
 KW Polymorphism.  
 FT SIGNAL 1 41  
 FT CHAIN 42 941  
 FT  
 FT DOMAIN 42 483  
 FT TRANSMEM 484 504  
 FT DOMAIN 505 522  
 FT TRANSMEM 523 543  
 FT DOMAIN 544 551  
 FT TRANSMEM 552 572  
 FT DOMAIN 573 597  
 FT TRANSMEM 598 618  
 FT DOMAIN 619 654  
 FT TRANSMEM 655 675  
 FT DOMAIN 676 691  
 FT TRANSMEM 692 712  
 FT DOMAIN 713 720  
 FT TRANSMEM 721 741  
 FT DOMAIN 742 941  
 FT DOMAIN 781 819  
 FT CARBOHYD 90 90  
 FT CARBOHYD 298 298  
 FT CARBOHYD 389 389  
 FT CARBOHYD 404 404  
 FT CARBOHYD 453 453  
 FT VARSPLIC 902 927  
 FT VARSPLIC 929 941  
 FT  
 FT VARIANT 628 628  
 FT  
 FT VARIANT 869 869  
 FT  
 FT VARIANT 869 869  
 FT  
 FT CONFLICT 6 6  
 FT CONFLICT 12 12  
 FT CONFLICT 424 424  
 FT  
 FT SEQUENCE 941 AA; 105821 MW; 09F173DB0673C5D CRC64;  
 SO  
 Query Match 7.28; Score 89.5; DB 1; Length 941;  
 Best Local Similarity 44.18; Pred. No. 5.1;  
 Matches 26; Conservative 2; Mismatches 22; Indels 9; Gaps 3;  
 Oy 170 SPRPLEATAPAPPP-----LLLLLLPVGLLLAAACMLHWRTTRRTTTPRGQVPPV 224  
 Db 3 SPRSSGQGPPIPPPPPPPPPARLLLLLLPLPLPLAAGW--GW---AKGAPRPPSSPPL 56  
 ID SCGA\_MESAU STANDARD; PRT; 387 AA.  
 AC Q64255;  
 DT 20-AUG-2001 (Rel. 40, Created)  
 DT 20-AUG-2001 (Rel. 40, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE ALPHA-SARCOGLYCAN PRECURSOR (ALPHA-SG) (ADHALLIN) (50 KDA DYSTROPHIN-  
 DE ASSOCIATED GLYCOPROTEIN) (50DAG).  
 GN SCGA.  
 OS Mesocricetus auratus (Golden hamster).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
 OC Mesocricetus.  
 CX NCBI\_TaxID=10036;  
 CX  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SYRIAN; TISSUE=Heart muscle;  
 RX MEDLINE=98054328; PubMed=9391120;  
 RA Sakamoto A., Ono K., Abe M., Jasmin G., Eki T., Murakami Y.,  
 RA Masaki T., Itoyo-Oka T., Hanaoka F.;

RT "Both hypertrophic and dilated cardiomyopathies are caused by mutation  
 RT of the same gene, delta-sarcoglycan, in hamster: an animal model of  
 RT disrupted dystrophin-associated glycoprotein complex."  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:13873-13878(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-FIB: TISSUE-Skeletal muscle;  
 RX MEDLINE=95278335; PubMed=7558576;  
 RA Roberds S.L., Campbell K.P.:  
 RA "Adhalin mRNA and cDNA sequence are normal in the cardiomyopathic  
 RT hamster."  
 RL FBS Lett. 364:245-249(1995).  
 CC -1- FUNCTION: COMPONENT OF THE SARCOGLYCAN COMPLEX, A SUBCOMPLEX OF  
 CC THE DYSTROPHIN-GLYCOPROTEIN COMPLEX WHICH FORMS A LINK BETWEEN THE  
 CC F-ACTIN CYTOSKELETON AND THE EXTRACELLULAR MATRIX.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN, SARCOLEMAL  
 CC (POTENTIAL).  
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN SKELETAL AND  
 CC HEART MUSCLE.  
 CC -1- SIMILARITY: BELONGS TO THE SARCOGLYCAN ALPHA/EPSILON FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D83651; BAA12025.1; -  
 DR EMBL: U21677; AAA81645.1; -  
 DR Cytokeleton: Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 23  
 FT CHAIN 1 23  
 FT DOMAIN 24 290  
 FT TRANSMEM 291 311  
 FT DOMAIN 312 387  
 FT DOMAIN 209 335  
 FT CARBOHYD 174 174  
 FT CARBOHYD 246 246  
 FT SEQUENCE 387 AA; 43326 MW; D8599C0FAF646C3F CRC64;  
 SO

Query Match 7.2%; Score 89; DB 1; Length 387;  
 Best Local Similarity 23.4%; Pred. No. 2;  
 Matches 71; Conservative 26; Mismatches 97; Indels 110; Gaps 14;

QY 11 TTYVLLLLSSGLSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPYVANSNLODEELC 70  
 DB 115 TTRQRLLLI-----EDPEGRLPYQAEFLVRSNDEVL-----PSTANRFL--TAL 161  
 QY 71 GGLMRL-----VLQRMERLKYAGSKMOGLLENVNEHFVT-----K 110  
 DB 162 GGLMELDELQLLNTTSALDRGRVRLPIEGKKEGVYIKVGSATPFSTCLKMWASPSYAR 221  
 QY 111 CAEQPP--SC-----LRFVQTNISRLQETSEQLVAKPWITRQNSFSCLEOCOPD 161  
 DB 222 CAQGPRLLSYDLSLAFHFRDMQCNVSLVKSYPEPD-----EYPPPGD 266  
 QY 162 SSTLPWPSPRPLEAT-----APTAPQRPRLLLLLPVLGLLLAAMC----- 204  
 DB 267 GLEHDFPFCPTREATGRDELADALVTLVPLVALL--TLLAYIMCCRREGOLKRD 323  
 QY 205 -----LHMQRTRRRTRP-----GEQVPP--VPSPQ--DLL 231  
 DB 324 MATSDIQMHCHTGHNTIELRQMAARREVPRLSTLPMFNVTGERLPPRVDSQVPLI 383  
 QY 232 LVFH 235  
 DB 384 LDQH 387

S3A1\_HUMAN  
 ID S3A1\_HUMAN STANDARD; PRT; 793 AA.  
 AC Q15459;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE SPLICING FACTOR 3 SUBUNIT 1 (SPLICOSOME ASSOCIATED PROTEIN 114) (SAP  
 DE 114) (SFA120).  
 GN SFA1 OR SAP114.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9607958; PubMed=7489498;  
 RA Kremer A., Mulhauser F., Wersig C., Groning K., Bilbe G.;  
 RT "Mammalian splicing factor SFA120 represents a new member of the  
 RT SURF family of proteins and is homologous to the essential splicing  
 RT factor PRP21p of Saccharomyces cerevisiae."  
 RL RNA 1:260-272(1995).  
 RL [2]  
 RP SEQUENCE FROM N.A.  
 RA Bentley D., Blandford M.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP CHARACTERIZATION OF THE SPLICOSOME.  
 RX PubMed=10882114;  
 RA Das R., Zhou Z., Reed R.;  
 RT "Functional association of U2 snRNP with the ATP-independent  
 RT spliceosomal complex E.";  
 RL Mol. Cell 5:779-787(2000).  
 CC -1- FUNCTION: SUBUNIT OF THE SPLICING FACTOR SFA3 REQUIRED FOR 'A'  
 CC COMPLEX ASSEMBLY FORMED BY THE STABLE BINDING OF U2 SNRNP TO THE  
 CC BRANCHPOINT SEQUENCE (BPS) IN PRE-MRNA. SEQUENCE INDEPENDENT  
 CC BINDING OF SFA3/SFB3 COMPLEX UPSTREAM OF THE BRANCH SITE IS  
 CC ESSENTIAL, IT MAY ANCHOR U2 SNRNP TO THE PRE-MRNA. MAY ALSO BE  
 CC INVOLVED IN THE ASSEMBLY OF THE 'E' COMPLEX.  
 CC -1- SUBUNIT: COMPONENT OF SPLICING FACTOR SFA3 WHICH IS COMPOSED OF  
 CC THREE SUBUNITS: SFA3A/SAP61, SFA3A2/SAP62, SFA3A1/SAP114. SFA3A  
 CC ASSOCIATES WITH THE SPLICING FACTOR SFB3 AND A 12S RNA UNIT TO  
 CC FORM THE U2 SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX (U2 SNRNP).  
 CC INTERACTS WITH SFA3.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.  
 CC -1- SIMILARITY: CONTAINS 1 UBQUITIN-LIKE DOMAIN.  
 CC -1- SIMILARITY: TO YEAST PRE-MRNA SPLICING FACTOR PRP21.  
 CC -----  
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 CC -----  
 DR EMBL: X85337; CA59494.1; -  
 DR EMBL: AC004997; AAC23435.1; -  
 DR MIM: 605595; -  
 DR InterPro: IPR000061; SURF.  
 DR InterPro: IPR000062; Ubiquitin.  
 DR Pfam: PF001805; Surp; 2.  
 DR Pfam: PF00240; ubiquitin; 1.  
 DR SMART: SM00213; UBQ; 1.  
 DR PROSITE: PS50053; UBQUITIN\_2; 1.  
 DR SPLICOSOME: mRNA processing; mRNA splicing; Nuclear protein; Repeat.  
 FT REPEAT 52 94  
 FT REPEAT 166 208  
 FT DOMAIN 707 793  
 FT DOMAIN 10 16  
 FT DOMAIN 118 122  
 FT DOMAIN 260 267  
 FT DOMAIN 369 372  
 FT POLY-PRO.

FT DOMAIN 557 560 POLY-PRO.  
FT DOMAIN 672 675 POLY-PRO.  
SO SEQUENCE 793 AA: 88886 MW: 725961EC4577305C CRC64;

Query Match 7.2%; Score 89; DB 1; Length 793;  
Best Local Similarity 22.3%; Pred. No. 4.6;  
Matches 67; Conservative 34; Mismatches 79; Indels 120; Gaps 17;

QY 4 LAPAMSPFTYLLLLLSGLSGTQDCSPHSPSSDFAVKIRELSYLLQDYVTVASN 63  
DB 401 LPPAPADELV-----SPITGE---KI-----PASK 424  
QY 64 LODELGGIMRLVLAQRME-RLKTV-----AGSKMQLLERYNTEIHF 107  
DB 425 MOEHMRIG-----LLDRRWLEQQRDSIREKQSDDEVAYAPGLDIESLKLQALR-RTDIFG 478  
QY 108 VTKCA-----FQPPSPCLNF-----VQTNISRLQETSQALVAKPMI 145  
DB 479 VESTATIGKKIGEERIOKPEEKVTWDGSHGSMARTQAQAQANIT--LOEOIEAIHKAGLV 536  
QY 146 -----TRONF--SRCLAQCCP-----DSSFLP-----PWSRPLEAT---APT 180  
DB 537 PEDDTKKTGPKSPKNEIPQPPPPSSATNIPSSAPITTSVPRPTMPPTVVSAPV 596  
QY 181 APOPELLLLLPVGLLLLAAMCLHMQR-----RRTPRGEQVPP---VSP 227  
DB 597 MPRPMASVVRLLPGSVIAPMPRIIHAPRINNVMPSPAPPIAPRPPMIVPAFVPAP 656  
RESULT 7  
TNC\_MOUSE  
ID TNC\_MOUSE STANDARD; PRT; 415 AA.  
AC P50284;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE LPHOTOXIN-BETA RECEPTOR PRECURSOR.  
GN LTBOR OR TNECR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-CVB: TISSUE=Lung;  
RC MEDLINE=96072804; PubMed=7594541;  
RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
RA Browning J.U., Ware C.F.;  
RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
RT and expression.";  
RL J. Immunol. 155:5280-5288(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=96163885; PubMed=8586432;  
RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
RA Honjo T.;  
RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
RT sequence trap and chromosomal mapping.";  
RL Genomics 30:312-319(1995).  
CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
CC IMMUNE DEVELOPMENT.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U29173; AAA68964.1; -  
DR EMBL: L38423; AAB00846.1; -  
DR EMBL: U30798; AAB1334.1; -  
DR HSSP: P25942; 1CDF.  
DR MGD: MGI:104875; Ltbr  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 3.  
DR Prodom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR; 3.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 415  
FT DOMAIN 31 223  
FT TRANSMEM 224 244  
FT DOMAIN 245 415  
FT DOMAIN 42 213  
FT REPEAT 42 81  
FT REPEAT 82 124  
FT REPEAT 125 170  
FT REPEAT 171 213  
FT DISULFID 43 58  
FT DISULFID 59 72  
FT DISULFID 62 80  
FT DISULFID 83 98  
FT DISULFID 101 116  
FT DISULFID 104 124  
FT DISULFID 126 132  
FT DISULFID 139 150  
FT DISULFID 142 169  
FT DISULFID 172 187  
FT CARBOHYD 40 40  
FT CARBOHYD 179 179  
SQ SEQUENCE 415 AA: 44956 MW: 298326A566AEF661 CRC64;

Query Match 7.0%; Score 87.5; DB 1; Length 415;  
Best Local Similarity 24.4%; Pred. No. 2.9;  
Matches 39; Conservative 20; Mismatches 52; Indels 49; Gaps 8;

QY 110 KCAFQPPPSCL-----RFV-----QTNISRLQETSQALVAKPMITRONFS 151  
DB 123 ECRQCPGMSCVYLDNCEVHCEERLYLCQPTAEVYDEIMTDVNCVPCPGHQTSS 182  
QY 152 RCLLEQCPDSSSTLPWSPRPLEATAP-----TAPPELLLLLPVGLL--- 198  
DB 183 P--RARCQPHTRC-----EIQGLVEAPAGTSYSDTICKNPPRGAMLLAILSLVFL 235  
QY 199 ----LAAWCLHMQR-----RRTPRGEQVPPVPSQ 228  
DB 236 FTVYVLAACAMMRHPSLCRKLTGLTKRHPE-GEESPCCAPR 274  
RESULT 8  
MPID\_DROME  
ID MPID\_DROME STANDARD; PRT; 479 AA.  
AC P20483; Q9VAL9;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 20-AUG-2001 (Rel. 40, Last sequence update)  
DT 20-AUG-2001 (Rel. 40, Last annotation update)  
DE M-PHASE INDUCER PHOSPHATASE (EC 3.1.3.48) (STRING PROTEIN) (CDC25-LIKE  
DE PROTEIN).  
GN STG OR CDC25 OR CG1395.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=89195217; PubMed=2702688;  
RA Edgar B.A., O'Farrell P.H.;



```

CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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CC -----
DR EMBL: L26525; AAA21089.1; -.
DR HSSP: P11362; 1FG1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR002011; Reptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00754; F5_F8_type_C; 1.
DR Pfam: PF00069; Kinase; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00239; RECEPTOR_KINASE_TYR; 1.
DR PROSITE: PS01285; FA58C_1; 1.
DR PROSITE: PS01286; FA58C_2; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Tyrosine-protein kinase; Glycoprotein; Signal;
KW Phosphorylation; Transmembrane; Receptor; ATP-binding.
FT SIGNAL 1 19
FT CHAIN 20 910
FT DOMAIN 20 413
FT TRANSMEM 414 440
FT DOMAIN 441 910
FT DOMAIN 32 186
FT FT 378 412
FT DOMAIN 473 598
FT DOMAIN 607 902
FT NE_BIND 613 621
FT BINDING 652 652
FT ACT SITE 763 763
FT DISULFID 32 186
FT MOD_RES 510 510
FT MOD_RES 789 789
FT MOD_RES 793 793
FT MOD_RES 794 794
FT CARBOHYD 212 212
FT CARBOHYD 261 261
FT CARBOHYD 371 371
FT CARBOHYD 391 391
SQ SEQUENCE 910 AA; 101164 MW; 7E7FFAIDCB029806 CRC64;

Query Match 7.03; Score 87; DB 1; Length 910;
Best Local Similarity 24.58; Pred. NO. 8;
Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

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ID DDRL_MOUSE STANDARD; PRT; 911 AA.
AC Q03146;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE EPITHELIAL DISCOLDIN DOMAIN RECEPTOR 1 PRECURSOR (EC 2.7.1.112)
DE (TYROSINE-PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE
DE DOR) (DISCOLDIN RECEPTOR TYROSINE KINASE) (PROTEIN-TYROSINE KINASE
DE MK-6).
GN DDRL OR EDDRL OR CAK OR MPK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL.
RX MEDLINE=96204002; PubMed=8622863;
RA Perez J.L., Jing S.Q., Wong T.W.;
RT "Identification of two isoforms of the Cak receptor kinase that are
RT coexpressed in breast tumor cell lines.";
RL Oncogene 12:1469-1477(1996).
RN [2]
RP SEQUENCE OF 766-822 FROM N.A.
RC STRAIN=C57BL; TISSUE=Embryonic brain;
RX MEDLINE=93096484; PubMed=1281307;
RA Gillardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G.,
RA Chester A., Wilkinson D.G., Charney P.;
RT "An Eph-related receptor protein tyrosine kinase gene segmentally
RT expressed in the developing mouse hindbrain.";
RL Oncogene 7:2499-2506(1992).
CC -1- FUNCTION: MAY BE INVOLVED IN CELL-CELL INTERACTIONS AND
CC RECOGNITION (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
CC PROTEIN TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; CAK I (SHOWN HERE) AND CAK II;
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER BY THE
CC ABSENCE OF A 37 RESIDUES SEGMENT.
CC -1- TISSUE SPECIFICITY: THE PREDOMINANT ISOFORM CAK I, IS EXPRESSED IN
CC DEVELOPING EMBRYO AND ADULT BRAIN; CAK II IS EXPRESSED IN VARIOUS
CC EPITHELIAL CELLS.
CC -1- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF TYR-PROTEIN
CC KINASES.
CC -1- SIMILARITY: CONTAINS 1 F5/8 TYPE C DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -----
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CC -----
DR EMBL: L57509; AAB05209.1; -.
DR EMBL: X57240; CAA40516.1; -.
DR PIR: S30502; S30502.
DR HSSP: P11362; 1FG1.
DR MGD: MGI:99216; Ddrl.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000421; FA58_C.
DR InterPro: IPR002011; Reptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00754; F5_F8_type_C; 1.
DR Pfam: PF00069; Kinase; 1.
DR SMART: SM00231; FA58C; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_APP; FALSE_NEG.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.

```



DR PROSITE; PS01285; FA58C.1; 1.  
 DR PROSITE; PS01286; FA58C.2; 1.  
 KM Transferase; Tyrosine-protein kinase; Glycoprotein; Signal;  
 KM Phosphorylation; Transmembrane; Receptor; ATP-binding;  
 KM Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 911  
 FT DOMAIN 20 414  
 FT TRANSMEM 415 441  
 FT DOMAIN 442 911  
 FT DOMAIN 32 186  
 FT DOMAIN 379 413  
 FT DOMAIN 474 599  
 FT DOMAIN 608 903  
 FT NP\_BIND 614 622  
 FT BINDING 653 653  
 FT ACT\_SITE 764 764  
 FT DISULFID 32 186  
 FT MOD\_RES 511 511  
 FT MOD\_RES 790 790  
 FT MOD\_RES 794 794  
 FT MOD\_RES 795 795  
 FT CARBOHYD 213 213  
 FT CARBOHYD 262 262  
 FT CARBOHYD 372 372  
 FT CARBOHYD 392 392  
 FT VARSPLIC 503 539  
 FT SEQUENCE 911 AA; 101160 MW; DBB/FE03DD/9510 CRC64;

POTENTIAL.  
 EPITHELIAL DISCOIDIN DOMAIN RECEPTOR 1.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 F5/8 TYPE C (PHOSPHOLIPID-BINDING, POTENTIAL).  
 GLY/PRO-RICH.  
 GLY/PRO-RICH.  
 PROTEIN KINASE.  
 ATP (BY SIMILARITY).  
 ATP (BY SIMILARITY).  
 BY SIMILARITY.  
 BY SIMILARITY.  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 MISSING (IN ISOFORM CAK II).  
 MISSING (IN ISOFORM CAK II).

Query Match 7.0%; Score 87; DB 1; Length 911;  
 Best Local Similarity 24.5%; Pred. No. 8;  
 Matches 38; Conservative 12; Mismatches 35; Indels 70; Gaps 9;

QY 143 PWITRONSRCLELQCPDSSTLP-PW---SPRPLEATA---PTAPQ-----184  
 DB 357 PWLSEISFISDV-VNDSDFPPAPWMPGPPPTNFSLEPRGQPVAKAEGSPTA 415  
 QY 185 -----PLLLLLLPVGLLLAAMCLHWOR-----TRR-----T 214  
 DB 416 ILIGLVAILLLLLLIALML-----WRLMRLLSKAERVLLEELTVHLSVPGDTILIN 471  
 QY 215 PRGEQVPP-----VPSPODLL 232  
 DB 472 NRPGERPPPPYQPRRPRGTPPHSAPCVNGSALL 506

RESULT 11  
 ID CNG4\_BOVIN STANDARD: PRT: 1394 AA.  
 AC 028181: 028082: 003861;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 20-AUG-2001 (Rel. 40, Last annotation update)  
 DE 240 KDA PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL (CONTAINS: GLUTAMIC ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)).  
 DE CNG CHANNEL 4 (CNG-4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)).  
 GN CNG4 OR CNG4.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=96009859; PubMed=7546742;  
 RA Koerschen H.G., Illing M., Seifert R., Sestl F., Williams A.,  
 RA Gores S., Colville C., Mueller F., Dose A., Godde M., Molday L.,  
 RA Kaupp U.B., Molday R.S.;  
 RT "A 240 kDa protein represents the complete beta subunit of the cyclic nucleotide-gated channel from rod photoreceptor.";

RL Neuron 15:627-636(1995).  
 RN [2]  
 RP SEQUENCE OF 454-1394 FROM N.A.  
 RC TISSUE-Testis;  
 RA MEDLINE=96198098; PubMed=8626431;  
 RA Biel M., Zong X., Ludwig A., Sauter A., Hofmann F.;  
 RT "Molecular cloning and expression of the modulatory subunit of the cyclic nucleotide-gated cation channel.";  
 RL J. Biol. Chem. 271:6349-6355(1996).  
 RN [3]  
 RP SEQUENCE OF 1-590 FROM N.A.  
 RC TISSUE-Retina;  
 RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;  
 RL Submitted (xxx-1991) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBUNIT: FORMS FUNCTIONAL HETEROLOGIC CHANNELS WITH CNG3.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; CNG4C (SHOWN HERE), CNG4D AND CNG4E; ARE PRODUCED BY ALTERNATIVE SPLICING. CNG4D IS BY FAR THE MOST FREQUENT FORM (CNG4D:CNG4C:CNG4E = 20:2:1) IN TESTIS.  
 CC -1- TISSUE SPECIFICITY: RETINA, TESTIS, KIDNEY, HEART, AND BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL FAMILY.  
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 CC DR EMBL: X94707; CAA64367.1; -;  
 CC DR EMBL: M61185; AAA30536.1; -;  
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 CC DR InterPro: IPR000595; cNMP\_binding.  
 CC DR Pfam: PF00914; CNG\_membrane.1.  
 CC DR Pfam: PF00027; cNMP\_binding.1.  
 CC DR SMART: SM00100; cNMP.1  
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 CC DR PROSITE; PS01201; CNGP\_BINDING\_314; 1.  
 CC DR PROSITE; PS01202; CNGP\_BINDING\_315; 1.  
 CC DR PROSITE; PS01203; CNGP\_BINDING\_316; 1.  
 CC DR PROSITE; PS01204; CNGP\_BINDING\_317; 1.  
 CC DR PROSITE; PS01205; CNGP\_BINDING\_318; 1.  
 CC DR PROSITE; PS01206; CNGP\_BINDING\_319; 1.  
 CC DR PROSITE; PS01207; CNGP\_BINDING\_320; 1.  
 CC DR PROSITE; PS01208; CNGP\_BINDING\_321; 1.  
 CC DR PROSITE; PS01209; CNGP\_BINDING\_322; 1.  
 CC DR PROSITE; PS01210; CNGP\_BINDING\_323; 1.  
 CC DR PROSITE; PS01211; CNGP\_BINDING\_324; 1.  
 CC DR PROSITE; PS01212; CNGP\_BINDING\_325; 1.  
 CC DR PROSITE; PS01213; CNGP\_BINDING\_326; 1.  
 CC DR PROSITE; PS01214; CNGP\_BINDING\_327; 1.  
 CC DR PROSITE; PS01215; CNGP\_BINDING\_328; 1.  
 CC DR PROSITE; PS01216; CNGP\_BINDING\_329; 1.  
 CC DR PROSITE; PS01217; CNGP\_BINDING\_330; 1.  
 CC DR PROSITE; PS01218; CNGP\_BINDING\_331; 1.  
 CC DR PROSITE; PS01219; CNGP\_BINDING\_332; 1.  
 CC DR PROSITE; PS01220; CNGP\_BINDING\_333; 1.  
 CC DR PROSITE; PS01221; CNGP\_BINDING\_334; 1.  
 CC DR PROSITE; PS01222; CNGP\_BINDING\_335; 1.  
 CC DR PROSITE; PS01223; CNGP\_BINDING\_336; 1.  
 CC DR PROSITE; PS01224; CNGP\_BINDING\_337; 1.  
 CC DR PROSITE; PS01225; CNGP\_BINDING\_338; 1.  
 CC DR PROSITE; PS01226; CNGP\_BINDING\_339; 1.  
 CC DR PROSITE; PS01227; CNGP\_BINDING\_340; 1.  
 CC DR PROSITE; PS01228; CNGP\_BINDING\_341; 1.  
 CC DR PROSITE; PS01229; CNGP\_BINDING\_342; 1.  
 CC DR PROSITE; PS01230; CNGP\_BINDING\_343; 1.  
 CC DR PROSITE; PS01231; CNGP\_BINDING\_344; 1.  
 CC DR PROSITE; PS01232; CNGP\_BINDING\_345; 1.  
 CC DR PROSITE; PS01233; CNGP\_BINDING\_346; 1.  
 CC DR PROSITE; PS01234; CNGP\_BINDING\_347; 1.  
 CC DR PROSITE; PS01235; CNGP\_BINDING\_348; 1.  
 CC DR PROSITE; PS01236; CNGP\_BINDING\_349; 1.  
 CC DR PROSITE;





DT 15-DEC-1998 (Rel. 37, last sequence update)  
DT 20-AUG-2001 (Rel. 40, last annotation update)  
DE MAX BINDING PROTEIN MNT (FOX PROTEIN) (MYC ANTAGONIST MNT).  
GN MNT OR ROX.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RN TISSUE=Fetal brain;  
RC MEDLINE=97327566; PubMed=9184233;  
RX Meroni G., Raymond A., Alcalay M., Borsani G., Tanigami A.,  
RA Tonlonderei R., Lo Nigro C., Messali S., Zollo M., Ledbetter D.H.,  
RA Brent R., Ballabio A., Carozzo R.;  
RT "Rox, a novel bHLH2p protein expressed in quiescent cells that  
heterodimerizes with Max, binds a non-canonical E box and acts as a  
transcriptional repressor";  
RL EMBL J. 16:2892-2906(1997).  
RN [2]  
RN SEQUENCE FROM N.A.  
RX MEDLINE=98260677; PubMed=9598315;  
RA Nigro C.L., Venesio T., Raymond A., Meroni G., Alberici P.,  
RA Cainerca S., Enrico F., Stack M., Ledbetter D.H., Liscia D.S.,  
RA Ballabio A., Carozzo R.;  
RT "The human ROX gene: genomic structure and mutation analysis in human  
breast tumors";  
RL Genomics 49:275-282(1998).  
CC -! FUNCTION: BINDS DNA AS A HETERODIMER WITH MAX AND REPRESSES  
TRANSCRIPTION. BINDS TO THE CANONICAL E BOX SEQUENCE  
5'-CACGCG-3' AND, WITH HIGHER AFFINITY, TO 5'-CACGCG-3'.  
CC -! SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER  
BHLH PROTEIN. BINDS DNA AS AN HOMODIMER OR A HETERODIMER WITH MAX.  
CC -! SUBCELLULAR LOCATION: NUCLEAR.  
CC -! SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: X96401; CAA65265.1; -;  
DR EMBL: Y13440; CAA73851.1; -;  
DR EMBL: Y13441; CAA73851.1; JOINED.  
DR EMBL: Y13442; CAA73851.1; JOINED.  
DR EMBL: Y13443; CAA73851.1; JOINED.  
DR EMBL: Y13444; CAA73851.1; JOINED.  
DR MIM: 603039; -;  
DR InterPro: IPR003015; HLH\_Myc.  
DR InterPro: IPR001092; HLH\_dlm.  
DR Pfam: PF00010; HLH; 1.  
DR SMART: SMO0353; HLH; 1.  
DR PROSITE: PS00036; HELIX\_LOOP\_HELIX; FALSE\_NEG.  
KW Transcription regulation; Repressor; Nuclear protein; DNA-binding.  
FT DNA\_BIND 222 233 BASIC DOMAIN.  
FT DOMAIN 234 270 HELIX-LOOP-HELIX MOTIF (POTENTIAL).  
FT DOMAIN 271 299 LEUCINE-ZIPPER.  
SQ SEQUENCE 582 AA; 62299 MW; 06AC320D79BF18A0 CRC64;

Query Match 6.88; Score 84; DB 1; Length 582;

Best local Similarity 21.18; Pred. No. 8.5;  
Matches 61; Conservative 35; Mismatches 89; Indels 104; Gaps 13;

QY 4 LAPAWSTTILLILLISS-----GLSGTQDCSFQHSPISSDFAVKIRELSDY 51  
Db 186 LAPQPPPTLGLTKLAPAEVKSSEQKRRPGGIGTREV--HNKLEKNRAHLKECFET 242  
QY 52 FLQDYPTVASNLODELGGIMRLVLAQRMEKLTIVAGSKMGLLEVRVTEIHFVTKC 111

Db 243 LKRNIP-----NDDKR-TSNLSVLRALRYIOGLKR-KEKEYEHMERLARE-----KI 290  
QY 112 AFQPPPSCLRFVQTNISRLQETSEQLVALKPTTRQNFSCLELOCPD----- 161  
Db 291 A-----TQRLAEHLKHELISO-----WMDVLEIDRVLRQTOQPEDDASTAS 333  
QY 162 -----SSTLPPP-MSPRELEATPAPQPPDLLL 189  
Db 334 EGEDNIDEDMEDRAGLGPPKLSHRPQPELLKSTLPPSTTPAPL-----PPNPHH----- 385  
QY 190 LILPVGILLILAAAMCLIMQRTRRRTPRRGVPP-----VSPQDLL 231  
Db 386 ---PHSVALLPPAHLVVOQQQPPQKTPLPAPPPPPAPAPQTLVPAHAHLV 431

Search completed: April 1, 2002, 06:27:05  
Job time: 626 sec

Mon Apr 1 06:15:19 2002

us-08-162-407-6.rsp

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Db 181 APQAPRLILLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

# RESULT 2

09MZ09 PRELIMINARY; PRT; 291 AA.

AC 09MZ09

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DE FL13 LIGAND.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

OX NCBI\_TaxID=9685;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20358731; PubMed=10902925;

RA Yang S., Sim G.K.;

RT "Molecular cloning of canine and feline flt3 ligand reveals high

RT degree of similarity to the human and mouse homologue but uniquely

RT long cytoplasmic domain."

RL DNA Seq. 11:163-166(2000).

DR EMBL: AF155149; AAF87089.1; -

SO SEQUENCE 291 AA; 32459 MW; 8F85A10A5EA0DC6 CRC64;

Query Match 72.0%; Score 894.5; DB 6; Length 291;

Best Local Similarity 80.5%; Pred. No. 8.1e-77;

Matches 178; Conservative 9; Mismatches 33; Indels 1; Gaps 1;

QY 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLDYDYPVT 60

Db 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLDYDYPVT 60

QY 61 ASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMOGLLEVNTEHFVTKCAFOPPESC 120

Db 61 ASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMOGLLEVNTEHFVTKCAFOPPESC 120

QY 121 RFVQTNISRLLOETSEOLVALKPMWTRONFSRCLELQCPDSSSTLPSPWSPRLEATAP 180

Db 121 RFVQTNISRLLOETSEOLVALKPMWTRONFSRCLELQCPDSSSTLPSPWSPRLEATAP 180

QY 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

QY 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

QY 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

QY 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

QY 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

QY 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 181 APOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Query Match 67.6%; Score 840; DB 6; Length 292;

Best Local Similarity 76.3%; Pred. No. 1.2e-71;

Matches 171; Conservative 12; Mismatches 37; Indels 4; Gaps 2;

QY 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLDYDYPVT 59

Db 1 MTVLAPAMSPPTTLLSSGSGTDCSFQHSPISSDFAVKIRELSYLDYDYPVT 59

QY 60 VASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMOGLLEVNTEHFVTKCAFOPPESC 119

Db 60 VASNLODEELCGGLMRLVLAQRMERLKTAVAGSKMOGLLEVNTEHFVTKCAFOPPESC 119

QY 61 VASNLODDKLCGAFWRVLAQRMGRRLKTAVAGSEMEKLELVNTEHFVTSCAFOPPLPSC 120

Db 61 VASNLODDKLCGAFWRVLAQRMGRRLKTAVAGSEMEKLELVNTEHFVTSCAFOPPLPSC 120

QY 120 LRFVQTNISRLLOETSEOLVALKPMWTRONFSRCLELQCPDSSSTLPSPWSPRLEATAP 179

Db 120 LRFVQTNISRLLOETSEOLVALKPMWTRONFSRCLELQCPDSSSTLPSPWSPRLEATAP 179

QY 121 LRFVQTNISRLLOETSEOLVALKPMWTRONFSRCLELQCPDSSSTLPSPWSPRLEATAP 180

Db 121 LRFVQTNISRLLOETSEOLVALKPMWTRONFSRCLELQCPDSSSTLPSPWSPRLEATAP 180

QY 180 TAPOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

Db 180 TAPOPP--LLLLLLPVGILLAAWCLHMQRTRRRTPRPEQ 220

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

QY 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236

Db 181 PGQSPPLLLLLLPVALLMSTAWCLHWRRRRRRRRSPYGEORITLRPESRSHLPED 236







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Db 76:PPGPPRLPCSGSTPPGRLLPQ-----ALAPPGHGFSS--RFWHNPTTQAPPG 127
Oy 170 SPRPL-EATAP-----TAPQPLLLLLLVGLLLAAACLMQRTTTPPG 218
    ||| : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 128 PPRPLPQALVPPQDHPGSSPTTQAPPL-----W-LHPRTT--OTPPG 169
Oy 219 EGVPPVPSQDUL-LVEH 235
    || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 170 ---PPRPLPQALPQLQDH 164

RESULT 11
O9PU36 PRELIMINARY: PRT: 5120 AA.
AC O9PU36:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ACZONIN (FRAGMENT).
GN AC2.
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99439764; PubMed=10508862;
RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,
RT "Kilimann M.W.;
RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active
RT zones, shares homology regions with rim and bassoon and binds
RT profilin.";
RL J. Cell Biol. 147:151-162(1999).
DR EMBL: Y19187; CAB60725.1; -.
DR HSSP: P04410; 1A25.
DR InterPro: IPR000008; C2.
DR InterPro: IPR001478; PDZ.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR001565; Synaptotagmin.
DR Pfam: PF00168; C2; 2.
DR Pfam: PF00595; PDZ; 1.
DR PRINTS: PRO0360; C2DOMAIN.
DR PRINTS: PRO1217; PRICHEXTENS.
DR PRINTS: PRO0399; SYNAPTOTAGMN.
DR SMART: SM00239; C2; 2.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS00499; C2_DOMAIN_1; UNKNOWN_1.
DR PROSITE: PS00004; C2_DOMAIN_2; 2.
DR PROSITE: PS50106; PDZ; 1.
DR NON_TER 1
FT SEQUENCE 5120 AA; 560760 MW; A658D9891B65B412 CRC64;
SQ
```

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Query Match 7.3%, Score 90.5; DB 13; Length 5120;
Best Local Similarity 24.3%, Pred. No. 22;
Matches 45; Conservative 19; Mismatches 72; Indels 49; Gaps 7;
```

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Oy 90 AGSKQGLLEVRNTEIHF-----VTKCAFQPPPSCLRFVQTN----- 126
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2224 AARKKSTVEGILIKIHEDSHKELSLDMTRINTGATSEQPLCVASVKEPASETPA 2283
Oy 127 --ISLLDETSE-QVALAKPWITRONF-----SRCLDQCQPPSSTLPPWSPRLPEATAP 179
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2284 VPTPRVSKSTVSMPSAPALTSKVSLSFRSSSLDSPAQPPSPPPPPPPPLPP 2343
Oy 180 TAPQ-----PLLLLLLPVGLLLAAAWCLH--MQRTTTPPGECV 221
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 2344 ILPKVAIVPKKSOIQAPRAATPVAIVLTVSATLESAAVILKNHVPYTKTTPTPP-PPV 2402
Oy 222 PPVPS 226
    | | |
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Db 2403 PPKPS 2407

RESULT 12
ID 017610 PRELIMINARY: PRT: 474 AA.
AC 017610:
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE C28D4.2 PROTEIN.
GN C28D4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Rhabdilitidae;
OC Rhabdilitae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA McMurtry A.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL: Z82259; CAB05129.1; -.
DR InterPro: IPR002573; Choline_kinase.
DR Pfam: PF01633; Choline_kinase; 1.
SQ SEQUENCE 474 AA; 54628 MW; DDF1IC97A1542FFC CRC64;
```

```
Query Match 7.2%, Score 89.5; DB 5; Length 474;
Best Local Similarity 24.1%, Pred. No. 2.2;
Matches 59; Conservative 29; Mismatches 82; Indels 75; Gaps 15;
```

```
Oy 27 TDQC-----SFQHS-PISDFAVKIREL-SDVLDQYPYVASNLQDEELCGLWRL 76
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 TTDQVDLKKVFESKFPSSAPISSEILFRARFLCAKL-----GGARRK 106
Oy 77 VLAQRMERLKTAVASKQGLLEVRNTEIHFVTKCAFQPPPSCLR-FVQTNISRLQET- 134
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 107 VKIEEF--RIRAITGG-MSNLFLELPAH-LTPIQMEKALLHVHCQSDIDLQLESV 162
Oy 135 -----SQQLVALKPWITRONFNSRCLQC-----QPDSTLPPPSPP--PLEATA 178
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 163 VFTLLSERNLGPKMLGVPPGGRFEQFIPSRALQCEISKPGSLKILAPIVAHVHTLDAI 222
Oy 179 PTAQPPRLLLLLLVGLLLAAACLMQRTTTPP--RPGE-----QVPVPSPOD 229
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 PKEPQ-----TLQTAROWLERF-----KKTTPAGERIEMVLTQAKVPKSDYPT 266
Oy 230 LLIVE 234
    | | |
Db 267 ITVAQ 271
```

```
RESULT 13
O9UMT1 PRELIMINARY: PRT: 270 AA.
AC O9UMT1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE NKp4RG2 PROTEIN.
GN NKp4RG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Cantoni C., Biasoni R.;
RT "NKp4 related genes.";
RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
CC -I- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DR EMBL: AJ010100; CAB52290.1; -.
```

DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00409; Ig; 1.  
SQ SEQUENCE 270 AA; 29678 MW; 327AD57A5634AE46 CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 270;  
Best Local Similarity 23.0%; Pred. No. 1.5;  
Matches 63; Conservative 22; Mismatches 112; Indels 77; Gaps 15;

QY 7 AWSFTYLLLLLSGLSGTQDCSPQHSPISSDPAVKIRLSYLLQDYVTVASNLQD 66  
DB 2 AWRALHPLLLLLFPSSQAQKAVLQSVAGQTLVRCQ-----YPT----- 45  
QY 67 EELCGGLM-----RLVLAQR-----MMERLKTVAQSKMOGLLEVRNTEI- 105  
DB 46 -----GSLYEKKGCKEASALVCILVYSSKRMATWSRF-TIMDDDAGCFYTMIDL 100  
QY 106 -----HFVTKCAFQPPSCLEFVQTNISRLQETSEQLVAKPWITRONFSCLELQ-CQ 159  
DB 101 EEDSGHY--MCRIYRPSD--NSVSKSVRYLVSPASASTQTPTWPRDLVSSQTQSCV 156  
QY 160 PDS-----STLPPMSP-RELENTAPTAQ-----PRLLLLLLPV--GLL--- 197  
DB 157 PPTAGANQAPESPSTIPVSPHSPPLVPLSPRPNSTLRRPAPALVLPVFCGLLVAK 216  
QY 198 -LLAAMCLHMORTRRTPRPEQV--PVVSPQ 228  
DB 217 SLVSLALLVWVVLNRHMQHGRSLHRAQPRQ 250

RESULT 14  
Q9AMJ4 PRELIMINARY; PRT; 404 AA.  
AC 09AMJ4:  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DE 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE P0489A05.3 PROTEIN.  
GN P0489A05.3.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OC NCBI\_TaxID=4530;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC  
clone: p0489A05.";  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP003105; BAB32983.1; -  
SQ SEQUENCE 404 AA; 43109 MW; 7CA66FDE7772A64B CRC64;

Query Match 7.1%; Score 88.5; DB 10; Length 404;  
Best Local Similarity 26.1%; Pred. No. 2.3;  
Matches 66; Conservative 24; Mismatches 88; Indels 75; Gaps 17;

QY 33 QHSPISSDF--AVKIRELSYLLQDYVTVASNL-----ODEELCGGLMRLVL 78  
DB 107 RHFSLSEFLEKVOITPLKYVSMNYPLKPNQTFLLNRYQMKNSPEQLCKRFW---- 162  
QY 79 AQRMEERLKTVAQSKMOG--LLERVNT--EIHFTKCAFQPPSCLEFVQTNI---SRL 130  
DB 163 -STWQSNAGAV-GSRAGSERLRLRPSSAGRRPWLVPSPPPRASLAAGVYNALTSRA 220  
QY 131 LOETSEQLVAKPWITRONFSR---CLELQ--CQDPSSTLP-----PPWSRPLEAT 177  
DB 221 LSAAG-----TPTTSSSILRRPLHCLLPLRLARPPSPILPLQAPRHPLP---P 271

QY 178 APTAPQPELLLLLL-----PV---GLL-----LLAAMCLHMORTRRTPR 216  
DB 272 PPTARAPPPIAVLICLRCPLYLPKRPVAGGIFVAHSALTAVLCAGCV--RLHRRPLR 329  
QY 217 P--GEQVPPVPS 227  
DB 330 PPSELLPLSRAP 342

RESULT 15  
075064 PRELIMINARY; PRT; 1386 AA.  
ID 075064:  
AC 075064:  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)  
DE KIAA0476 PROTEIN.  
GN KIAA0476.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OC NCBI\_TaxID=9606;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RX MEDLINE=98116662; PubMed=9455484;  
RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,  
RA Nomura N., Ohara O.;  
RT "Characterization of cDNA clones in size-fractionated cDNA libraries  
from human brain.";  
RL DNA Res. 4:345-349(1997).  
DR EMBL: AB007945; BAA32321.1; -  
DR InterPro: IPR001194; DENN.  
DR InterPro: IPR002885; PPR.  
DR Pfam: PF01535; PPR; 1.  
DR Pfam: PF02141; DENN; 1.  
SQ SEQUENCE 1386 AA; 152296 MW; BE960E7169A7EFDA CRC64;

Query Match 7.1%; Score 88.5; DB 4; Length 1386;  
Best Local Similarity 23.1%; Pred. No. 8.6;  
Matches 53; Conservative 28; Mismatches 85; Indels 63; Gaps 12;

QY 21 SSGLSGTQDCSPQHSPISSDPAVKIRLSYLLQDYVTVASNLQDELC---GGLMRL 76  
DB 1104 SAGASGSKDAPVPGP-----GVLSDRRLCLA--LDEPQLCGHWGASRR 1148  
QY 77 VLAQRMEERLKTVAQSKMOGLLEVRNTEIHFTKCAFQPPSCLEFVQTNISRLQETSE 136  
DB 1149 VESGAMVYLSPLVLRKELESIVENEGSEV---LALPELSAHPITFMNLLMYFORL-- 1201  
QY 137 QLVAKPWITRONFSCLELQCC-PDSSSTLPPEW-SRPLEA-----TAPTAPQP 185  
DB 1202 RLPSILPLGLVLA-----CQSPSHQAQAPSWLITPDPAISVQYRLMDVLITPDPNSCP 1253  
QY 186 LLLLLLPVGLLLAAMCLHMORTRRTPRPEQVPPVSPDOLLIVE 234  
DB 1254 LYVL-----WRVHSQ-IQORVWPG---PVBASLSALLE 1284

Search completed: April 1, 2002, 06:25:43  
Job time: 619 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 77.69 Seconds  
(without alignments)  
224.060 Million cell updates/sec

Title: US-08-162-407-6

Perfect score: 1242

Sequence: 1 MTVLAPAWSPPTLYLLLL.....RPCGVPPVSPDQLLVEH 235

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_1101.\*  
1: /SID52/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
2: /SID52/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
3: /SID52/gcgdata/geneseq/geneseq/AA1982.DAT.\*  
4: /SID52/gcgdata/geneseq/geneseq/AA1983.DAT.\*  
5: /SID52/gcgdata/geneseq/geneseq/AA1984.DAT.\*  
6: /SID52/gcgdata/geneseq/geneseq/AA1985.DAT.\*  
7: /SID52/gcgdata/geneseq/geneseq/AA1986.DAT.\*  
8: /SID52/gcgdata/geneseq/geneseq/AA1987.DAT.\*  
9: /SID52/gcgdata/geneseq/geneseq/AA1988.DAT.\*  
10: /SID52/gcgdata/geneseq/geneseq/AA1989.DAT.\*  
11: /SID52/gcgdata/geneseq/geneseq/AA1990.DAT.\*  
12: /SID52/gcgdata/geneseq/geneseq/AA1991.DAT.\*  
13: /SID52/gcgdata/geneseq/geneseq/AA1992.DAT.\*  
14: /SID52/gcgdata/geneseq/geneseq/AA1993.DAT.\*  
15: /SID52/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
16: /SID52/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
17: /SID52/gcgdata/geneseq/geneseq/AA1996.DAT.\*  
18: /SID52/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
19: /SID52/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
20: /SID52/gcgdata/geneseq/geneseq/AA1999.DAT.\*  
21: /SID52/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID52/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	16	AA67541 Human flt-3 ligand
2	1242	100.0	235	20	AA67769 Human flt3-ligand
3	1242	100.0	235	21	AA69719 Full length wild t
4	1242	100.0	235	22	AA620192 Human flt-3 ligand
5	1236	99.5	235	16	AA66175 Human S86/s109 flt
6	1236	99.5	235	22	AA620194 Human flt-3 ligand
7	1114	89.7	212	21	AA69721 Human flt-3 recept
8	1114	89.7	209	19	AA69007 Mature wild type h
9	1114	89.7	209	21	AA69720 Human flt-3 mutcin
10	1110	89.4	209	21	AA69723 Human flt-3 mutcin
11	1110	89.4	209	21	AA69726 Human flt-3 mutcin

12	1110	89.4	209	21	AA69727 Human flt-3 mutcin
13	1110	89.4	209	21	AA69729 Human flt-3 mutcin
14	1108	89.2	209	21	AA69722 Human flt-3 mutcin
15	1108	89.2	209	21	AA69724 Human flt-3 mutcin
16	1107	88.6	209	21	AA69728 Human flt-3 mutcin
17	1100	89.1	209	21	AA69725 Human flt-3 mutcin
18	970	78.1	185	22	AA620195 Human flt-3 ligand
19	895.5	72.1	294	21	AA58204 Canine flt-3 ligand
20	894.5	72.0	291	21	AA58210 Peline flt-3 ligand
21	834	67.1	178	22	AA620193 Human flt-3 ligand
22	797.5	64.2	268	21	AA58206 Canine mature flt-
23	796.5	64.1	276	21	AA58207 Canine flt-3 ligand
24	791.5	63.7	265	21	AA58211 Feline mature flt-
25	768.5	61.9	231	16	AA67540 Mouse flt-3 ligand
26	768.5	61.9	231	20	AA67768 Murine flt3-ligand
27	768.5	61.9	231	22	AA620186 Mouse flt-3 ligand
28	768	61.8	232	16	AA66177 Mouse Mot10/T118
29	764	61.5	232	22	AA620189 Mouse flt-3 ligand
30	745	60.0	150	19	AA677930 Flt3 ligand FL10C
31	745	60.0	150	19	AA669054 Human flt-3 recept
32	740.5	59.6	377	19	AA678124 Chimeric receptor
33	739	59.5	143	19	AA677926 Flt3 ligand FL13C
34	739	59.5	143	19	AA69050 Human flt-3 recept
35	737.5	59.4	349	19	AA683289 Human flt3 ligand
36	737.5	59.4	349	19	AA678005 Flt3L 1-139/IG52b/
37	736.5	59.3	340	19	AA683291 Human flt3 ligand
38	736.5	59.3	349	19	AA683286 Human flt3 ligand
39	736.5	59.3	523	19	AA678008 Trimeric Flt3L-G-C
40	735	59.2	140	19	AA677911 Human flt3 ligand
41	735	59.2	140	19	AA69035 Human flt-3 recept
42	735	59.2	144	19	AA677928 Flt3 ligand FL14C
43	735	59.2	144	19	AA69052 Human flt-3 recept
44	735	59.2	313	19	AA683294 Human flt3 ligand
45	733.5	59.1	286	19	AA683303 Human flt3 ligand

#### ALIGNMENTS

RESULT 1					
ID	AA67541	standard: Protein: 235 AA.			
XX	AA67541:				
AC	AA67541:				
XX	05-AUG-1995	(first entry)			
XX					
DE	Human flt-3 ligand.				
XX					
KW	Flt-3 ligand; flt3-L; anemia; cancer; AIDS; gene therapy.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	Peptide	1..26			
FT		/label= Sig.peptide			
FT		/note= "signal peptide may extend to position 27"			
FT	Domain	27..182			
FT		/label= Extracellular-domain			
FT		/note= "extracellular domain may start at position 28"			
FT					
FT	Domain	183..205			
FT		/label= Transmembrane-domain			
FT	Domain	206..235			
FT		/label= Cytoplasmic-domain			
XX					
PN	EP627487-A.				
XX					
XX	07-DEC-1994.				
PD					
XX					
PF	19-MAY-1994:	94EP-030375.			
XX					
PR	24-MAY-1993:	93US-0068394.			

PR 12-AUG-1993; 93US-0106463.  
 PR 23-AUG-1993; 93US-0111758.  
 PR 03-DEC-1993; 93US-0162407.  
 PR 07-MAR-1994; 94US-0209502.  
 PR 11-MAY-1994; 94US-0243545.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Beckmann MP, Lyman SD;  
 DR WPI: 1995-008071/02.  
 DR N-PSDB; AAQ79079.  
 XX  
 PT Isolated ligands for flt 3 receptors - useful for treating  
 PT anaemia, AIDS and various cancers  
 PS  
 XX Disclosure; Page 29-30; 33pp; English.  
 CC  
 CC A human T-cell lambda-gli0 random primed cDNA library was  
 CC screened with a fragment corresponding to the extracellular  
 CC domain of mouse flt3 ligand (flt3-L) (nt 103-516 of AAQ79076)  
 CC to isolate human flt3-L cDNA. Flt-3 stimulates progenitor and  
 CC stem cells, and can be used e.g. in gene therapy protocols.  
 XX  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 1242; DB 16; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPYTV 60  
 Db 1 mtvalapawspptyllllllssgsgtqdcsfqhspsdsfavkirelsdyllqdyptv 60  
 QY 61 ASNQDELCGGLRWLYLAQRMRERLKTAVAGSKKQGLLEVNTEIHFTVKCAQPPPSCL 120  
 Db 61 asnqdeelcgglrwlylaqrmerlktvagskmgllervnteihvtkcatqpppscl 120  
 QY 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELCQPDSSFTLPPWSPRPLEATAPT 180  
 Db 121 rfvgtnisrllqetseqlvalkpwtitrgnfsrclelcqpdssclppwsprrleatapt 180  
 QY 181 APQPELLLLLLPYGLLLLAAAWCLHWQRTTRTPRGEQVPVPSQDILLVEH 235  
 Db 181 apqpplllllllpyglllllaawclhwgrtrtrtprgpqvppvpqdillveh 235  
 RESULT 2  
 AAM67769 standard; Protein; 235 AA.  
 XX ID AAM67769;  
 AC AAM67769;  
 XX  
 DT 25-MAR-1999 (first entry)  
 XX  
 DE Human flt3-ligand.  
 XX  
 KW Antigen-specific peripheral immune tolerance; flt3-ligand; flt3-L;  
 KW immunogenic; autoimmune disease; organ transplantation; food allergy;  
 KW tissue transplantation.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9857655-A1.  
 PN  
 PD 23-DEC-1998.  
 XX  
 PF 12-JUN-1998; 98WO-US12085.  
 XX  
 PR 17-JUN-1997; 97US-0877421.  
 XX  
 PA (IMMV ) IMMUNEX CORP.

XX  
 PI Abbott NM, Mowat AM, Viney JL;  
 XX  
 DR WPI: 1999-070422/06.  
 DR N-PSDB; AAV61506.  
 XX  
 PT Methods for initiating or enhancing antigen specific immune  
 PT tolerance - by using murine or human flt3 ligand  
 PS  
 XX Claim 1; Page 14-15; 25pp; English.  
 CC  
 CC A method has been developed of initiating or enhancing: (i) an antigen-  
 CC specific immune tolerance; or (ii) immunotolerance of a therapeutic  
 CC immunogenic molecule by addition of a polypeptide, before, after or with  
 CC the mucosal administration of an immunotolerising amount of the antigen  
 CC or therapeutic molecule, respectively. The polypeptide is capable of  
 CC binding the flt3 receptor and is: a) amino acids 28-x of murine flt3  
 CC ligand (flt3-L), where x is an amino acid between 163-231; b) amino  
 CC acids 28-y of human flt3-L, where y is an amino acid between 160-235;  
 CC and c) a polypeptide that has at least 90% identity to the polypeptides  
 CC of either (a) or (b). The method ameliorates the effects of autoimmune  
 CC diseases, food allergies or organ or tissue rejection following  
 CC transplantation. Administration of flt3-L allows lower doses of antigens  
 CC to be used in vivo for mucosally administered antigens. The present  
 CC sequence represents human flt3-L.  
 XX  
 SQ Sequence 235 AA;  
 Query Match 100.0%; Score 1242; DB 20; Length 235;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-109;  
 Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MTVALPAMSPPTTYLLLLSSGSGTQDCSFQHSPISSDFAVKIRELSYLLQDYPYTV 60  
 Db 1 mtvalapawspptyllllllssgsgtqdcsfqhspsdsfavkirelsdyllqdyptv 60  
 QY 61 ASNQDELCGGLRWLYLAQRMRERLKTAVAGSKKQGLLEVNTEIHFTVKCAQPPPSCL 120  
 Db 61 asnqdeelcgglrwlylaqrmerlktvagskmgllervnteihvtkcatqpppscl 120  
 QY 121 RFVQTNISRLQETSEDLVALKPWITRONFSRCLELCQPDSSFTLPPWSPRPLEATAPT 180  
 Db 121 rfvgtnisrllqetseqlvalkpwtitrgnfsrclelcqpdssclppwsprrleatapt 180  
 QY 181 APQPELLLLLLPYGLLLLAAAWCLHWQRTTRTPRGEQVPVPSQDILLVEH 235  
 Db 181 apqpplllllllpyglllllaawclhwgrtrtrtprgpqvppvpqdillveh 235  
 RESULT 3  
 AAY69719 standard; Protein; 235 AA.  
 XX ID AAY69719;  
 AC AAY69719;  
 XX  
 DT 05-JUL-2000 (first entry)  
 XX  
 DE Full length wild type human flt-3 protein.  
 XX  
 KW Immunomodulator; immunosuppressive; cytostatic; anti-anemic; anti-HIV;  
 KW neuroprotective; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
 KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
 KW cellular expansion; cellular differentiation; natural killer cell;  
 KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
 KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
 KW multiple myeloma; leukemia.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO200001823-A2.  
 PN  
 PD 13-JAN-2000.





Oy	121	RFWONINISLLEOTSEQLVAKLPWTRROFNSCLLEQCCPODSSSTLPPMSPPLEATAPT	180
Oy	121	RVGVNINISLLEOTSEQLVAKLPWTRROFNSCLLEQCCPODSSSTLPPMSPPLEATAPT	180
Db	121	rTvgvntnrltllgeteeeqvalkpwlrtqnfscrlcldgcqpsdstlppppspripileactpt	180
Oy	181	AFOPPLLLLLLLPVGILLAAAMCMLMORTRRRTTPRPSBQVPVPSPODLLVEH	235
Db	181	aqppllllllllllpvgillllaaawclhwgfrtrrrtpgsgevpvpspgdilllvhn	235
 RESULT 5			
ID	AAR6175	standard; Peptide: 235 AA.	
XX	AAR6175;		
AC	AAR6175;		
XX	10-AUG-1995	(first entry)	
DT	Human S86/S109 Flt3 ligand peptide sequence.		
DE	Human S86/S109 Flt3 ligand peptide sequence.		
XX	Flt3 ligand; tyrosine kinase receptor ligand.		
KW	Homo sapiens.		
OS	MO9426891-A.		
PN	24-NOV-1994.		
XX	18-MAY-1994;	94WO-US05150.	
PE	19-MAY-1993;	93US-0065231.	
XX	07-JUL-1993;	93US-0089263.	
PR	16-JUL-1993;	93US-0092549.	
PR	13-AUG-1993;	93US-0106340.	
PR	24-AUG-1993;	93US-0112391.	
PR	19-NOV-1993;	93US-0155111.	
PR	03-DEC-1993;	93US-0162413.	
XX	(INRM ) INST NAT SANTE & RECH MEDICALE.		
PA	(SCHE ) SCHERING CORP.		
XX	Birnbaum D, Culpepper JA, Hannum CH, Lee FD;		
DR	N-PSDB; AAO79642.		
XX	New ligand for the Flt3 tyrosine kinase receptor - and related		
PT	nucleic acid, vectors, host cells and antibodies, useful for		
PT	treating abnormal cell physiology and proliferation, e.g. cancer,		
PT	also for diagnosis and drug screening		
XX	Claim 11; Page 76-77; 90pp; English.		
XX	A CDNA library from the human stromal cell line 2S3V48, in		
CC	pME18S, was screened with an 800 bp fragment derived from		
CC	pME18S, clone T118. This fragment encompasses the coding region		
CC	conserved between two mouse clones, T118 and T110. Approx. 20		
CC	positive clones were selected and partially sequenced. Two		
CC	clones, S86 and S109, were found to be approx. 75% homologous		
CC	to the mouse clones over the first 163 AAs. Clone S86 continued		
CC	to show homology to T110 until the stop codon, although to a		
CC	lesser degree, for an overall homology of 66%. Clones T118 and		
CC	S109 do not show homology to each other or to the other clones		
CC	after mouse residue 163 (human residue 160). An additional mouse		
CC	clone designated MB8 has a 29 AA insert at the junction between		
CC	the common and divergent portions of the mouse ligand.		
XX	Sequence 235 AA:		
SO	Query Match	99.5%; Score 1236; DB 16; Length 235;	
	Best Local Similarity	99.6%; Pref. No. 1,3e+108;	
	Matches 234%, Conservative	0; Mismatches 1; Indels 0; Gaps 0;	

Accession	Protein	Gene	Species	Length	Weight	PI	Inst	Source	Comment
QY	1	MTVLAPAWSPPTVYLIIIIIISSGLSGTQDPCFQHPSTSSDFAVKIRELSDYLLQDYPVT	Human	60	6000	5.5	1	GenBank	
Db	1	mtvlapawspptyllylllllssglsqtdcsqhnpsissdfavkirelsdyllqdyptv	Human	60	6000	5.5	1	GenBank	
QY	61	ASNLDQDEBLGGLMRLVLAORMMERLKTVAAGSKMGLERVNTETIEFTVKAFAQPPPSCL	Human	120	12000	5.5	1	GenBank	
Db	61	asnldqeelcgalmrlvllaqrmmrerkltvagskmgl1lervntetieftvkaifqpppscl	Human	120	12000	5.5	1	GenBank	
QY	121	RFVQTNISRLQETSEQVALKWKITRONFSKLELQCPDSDSTLPPEWSPPELEATPT	Human	180	18000	5.5	1	GenBank	
Db	121	rftvqtnisrltqeseqvalkpwitrtqnfstclelqcpdsscltppwspripeatpt	Human	180	18000	5.5	1	GenBank	
QY	181	APOPELLLLLLPGLLLAAAWCLIMORRRRTPPGQVPPVPSPODLLVEN	Human	235	23500	5.5	1	GenBank	
Db	181	apqppllllllllpvglllllaawclimwqtrrttrtpipeqvppvpspdlllven	Human	235	23500	5.5	1	GenBank	
RESULT	6								
AAB20194	ID	AAB20194	standard; Protein; 235 AA.						
XX	XX	AAB20194;							
XX	XX	14-MAY-2001 (first entry)							
XX	XX	Human Flt-3 ligand.							
XX	XX	Flt-3 ligand; Fms-like tyrosine kinase; human; vaccine;							
XX	XX	immunotherapy; therapy; tumour; cancer; melanoma; glioma;							
XX	XX	lymphoma; autoimmune disease; infection; gene therapy.							
OS	XX	Homo sapiens.							
XX	XX	Key	Location/Qualifiers						
EH	FT	Peptide	1..26						
FT	FT	/label= Signal_peptide	27..235						
FT	FT	Protein	/label= Mature_protein	27..182					
FT	FT	Domain	/label= Extracellular_domain	183..205					
FT	FT	Domain	/label= Transmembrane_domain	206..235					
FT	FT	Domain	/label= Cytoplasmic_domain						
XX	XX	MO200109303-A2.							
XX	XX	08-FEB-2001.							
XX	XX	31-JUL-2000; 2000MO-US20679.							
XX	XX	30-JUL-1999; 99US-0146170.							
XX	XX	(VIC- ) VICAL INC.							
XX	XX	Hermanson GG;							
XX	XX	WPI: 2001-123319/13.							
XX	XX	N-PSDB; AAF30312.							
XX	XX	Immunogenic compositions comprising Flt-3 ligand encoding							
XX	XX	polynucleotide and one or more antigen, or cytokine encoding							
XX	XX	polynucleotides, useful for suppressing tumour growth and for							
XX	XX	autoimmune diseases (e.g. rheumatoid arthritis) -							
XX	XX	Claim 2; Page 137-138; 149pp; English.							
XX	XX	The present sequence is that of human Fms-like tyrosine kinase							
XX	XX	(Flt-3 ligand). The invention is directed to enhancing the							
XX	XX	immune response of a vertebrate to an antigen or a cytokine by							
XX	XX	administering in vivo, into a tissue of a vertebrate, a Flt-3							
XX	XX	ligand-encoding polynucleotide, and 1 or more antigen- or							

CC cytokine-encoding polynucleotides. The Flt-3 ligand-encoding  
CC polynucleotide may encode the present full-length human Flt-3  
CC ligand polypeptide, or amino acids 27-185, 1-185, 27-235 or 1-235  
CC of the Flt-3 ligand. The polynucleotides are incorporated into  
CC the cells of the vertebrate in vivo, and a prophylactically or  
CC therapeutically effective amount of Flt-3 ligand and 1 or more  
CC antigens or cytokines is produced in vivo. Pharmaceutical  
CC compositions comprising the polynucleotides are useful for  
CC suppressing tumour growth in a mammal. The tumour is melanoma,  
CC glioma or lymphoma, particularly B-cell lymphoma. They can also  
CC be used for the prophylactic and/or therapeutic treatment of:  
CC (a) bacterial (e.g. Bacillus infections), viral (e.g. hepatitis B  
CC and C in humans), parasitic (e.g. malaria) and fungal infections;  
CC (b) autoimmune diseases (e.g. rheumatoid arthritis and  
CC osteoarthritis); (c) cancer; and (d) Aujeszky's disease in pigs.  
CC Various other examples of these diseases are given in the  
CC specification.  
CC  
CC  
SQ Sequence 235 AA;

Query Match 99.5%; Score 1236; DB 22; Length 235;  
Best Local Similarity 99.6%; Pred. No. 1.3e-108;  
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTVLAPAMSPPTVLLLLSSGLSGTQDSFQHSPISSDFAVKIRELSDYLLQDYPVTV 60  
DB 1 mvtlapawspptyllllllssglsqgdcsgfshpslssdfavkirelsdylldqypvtv 60

QY 61 ASNLODEELCGMLRWLYLAQRMERLKTAVAGSKMOGLLELVNTEIHFTVKCAFQPPPSCL 120  
DB 61 asnlodeelcgalmrwlylaqrmerlktavagskmgllervnteihftvkcafqpppscl 120

QY 121 RFVQNTNISRLLQETSEQLVAKPWITRQNFRCLELQCPQSSFTLPWPWSRPLEATAPT 180  
DB 121 rfvqntnistrllqetseqlvalkpwtirqnfrclelqcpqssftlpwpwsrpleatapt 180

QY 181 APQPLLLLLLLPYGLLLAAAMCLHMQRTRRRTPRCEQVPPVSPQDLLVEH 235  
DB 181 apqpplllllllpygllllaaamclhmqrtrrrtrrrprpgeqvpvpspdqdllveh 235

RESULT 7  
AAV69721 ID AAV69721 standard; Protein; 212 AA.  
XX  
AC AAV69721;  
XX  
DT 05-JUL-2000 (first entry)  
XX  
DE Human flt-3 muteln L-3H.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; anti-neuroproliferative; anti-allergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; muteln.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
PN W0200001823-A2.  
XX  
PD 13-JAN-2000.  
XX  
PF 25-JUN-1999; 99WO-US14296.  
XX  
PR 02-JUL-1998; 98US-0109100.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX

PI Gradis TV, McGrew JT;  
XX  
DR WPI: 2000-182115/16.  
XX  
PT Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
PT contains amino acid substitutions at positions 8, 84, 118 or 122 -  
PS Claim 4; Page 79-80; 90pp; English.  
XX  
XX The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L.  
CC polypeptides. This sequence represents an example of the novel flt-3  
CC ligands and comprises the L-3H mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
SQ Sequence 212 AA;

Query Match 90.5%; Score 1124; DB 21; Length 212;  
Best Local Similarity 100.0%; Pred. No. 4.2e-98;  
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 SGTQDCSFQHSPISSDFAVKIRELSDYLLQDYPVVASNLODEELCGMLRWLYLAQRME 84  
DB 2 sgtqdcsgfshpslssdfavkirelsdylldqypvvasnlddeecgmlrwlylaqrme 84

QY 85 RLKTVAGSKMOGLLELVNTEIHFTVKCAFQPPPSCLRFVQNTNISRLLQETSEQLVAKPW 144  
DB 85 rlktvagskmgllervnteihftvkcafqpppsclrfvqntnistrllqetseqlvalkpw 144

QY 145 ITRQNFRCLELQCPQSSFTLPWPWSRPLEATAPTAPQPLLLLLLLPYGLLLAAAMC 204  
DB 145 itrqnfrclelqcpqssftlpwpwsrpleataptapqpplllllllpygllllaaawc 204

QY 205 LHMQRTRRRTPRCEQVPPVSPQDLLVEH 235  
DB 205 lhmqrtrrrtrrrprpgeqvpvpspdqdllveh 235

RESULT 8  
AAW69007 ID AAW69007 standard; peptide; 209 AA.  
XX  
AC AAW69007;  
XX  
DT 01-OCT-1998 (first entry)  
XX  
DE Human flt-3 receptor agonist.  
XX  
KW Human; flt-3 receptor agonist; hematopoietic cell stimulation; cancer;  
KW bone marrow reconstruction; haematological disease; immune deficiency;  
KW drug-induced myelosuppression; renal dialysis; gene therapy; infection;  
KW congenital metabolic disease; neurological disease; therapy;  
KW dendritic cell production.  
XX  
XX Homo sapiens.  
OS  
XX  
PN W09818923-A1.  
XX  
PD 07-MAY-1998.



AAV69723 147  
ID AAV69723 standard; Protein: 209 AA.  
XX  
AC AAV69723;  
XX  
DT 05-JUL-2000 (first entry)  
XX  
DE Human flt-3 mutein K84E.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; antitumor; anti-HIV;  
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutein.  
XX  
KW Homo sapiens.  
OS Synthetic.  
OS  
PN WO200001823-A2.  
PN 13-JAN-2000.  
PD  
XX 25-JUN-1999; 99WO-US14296.  
PF  
XX 02-JUL-1998; 98US-0109100.  
PR  
XX (IMMV ) IMMUNEX CORP.  
PA  
PI Graddis TJ, McGrew JT;  
XX WPI: 2000-182115/16.  
DR  
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
XX contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
PS Claim 4; Page 84-85; 90pp; English.  
XX  
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
CC polypeptides. This sequence represents an example of the novel flt-3  
CC ligands and comprises the K84E mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
XX Sequence 209 AA;  
SQ

Query Match 89.4%; Score 1110; DB 21; Length 209;  
Best Local Similarity 99.5%; Pred. No. 8.5e-97;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TQDCSFQHSPISSDPFAVKIRIELSDYLDQVYTVASNLQDEELCGGLRWLVLAQRMERL 86  
DB 1 tqdcsfqhspsissdfavkirelsdyllqdyptvasnlqdeelcgglwrlvlaqrmerl 60  
OY 87 KTVASGSKMOGLIERVNTIEHFVTKCARQPPSCLEFVQNTISRLQESSEQVALKPWT 146  
DB 61 ktvasgskmgllervnteihfvtkcarpppscltfvqntisrllqesseqvialkpwit 120

OY 147 RQNFSCLELQCCPDSSSTLPMPSPRLPEATAPTAPQPELLLLLLPYGLLLLAAAMCLH 206  
DB 121 rqnfscllelqcqpdssstlppsprrlpleataptapqpplllllpyglllilaawclh 180  
OY 207 WQTRRRRTPRPGEQVPPVPSQDLLLLVH 235  
DB 181 wqtrrrtrprpgeqvppvpsqddlllvh 209

RESULT 11  
AAV69726  
ID AAV69726 standard; Protein: 209 AA.  
XX  
AC AAV69726;  
XX  
DT 05-JUL-2000 (first entry)  
XX  
DE Human flt-3 mutein Q122R.  
XX  
KW Immunomodulator; immunosuppressive; cytostatic; antitumor; anti-HIV;  
KW neuroprotective; antiallergic; flt3 ligand; flt3-L; wild type; allergy;  
KW cell surface tyrosine kinase receptor; hematopoietic progenitor cell;  
KW cellular expansion; cellular differentiation; natural killer cell;  
KW cancer; dendritic cell; immune response; autoimmunity; immunosuppression;  
KW myelodysplasia; aplastic anemia; HIV infection; lymphoma; neuroblastoma;  
KW multiple myeloma; leukemia; mutein.  
XX  
OS Homo sapiens.  
OS Synthetic.  
PN WO200001823-A2.  
PN 13-JAN-2000.  
PD  
XX 25-JUN-1999; 99WO-US14296.  
PF  
XX 02-JUL-1998; 98US-0109100.  
PR  
XX (IMMV ) IMMUNEX CORP.  
PA  
PI Graddis TJ, McGrew JT;  
XX WPI: 2000-182115/16.  
DR  
XX Mutant soluble flt3 ligand polypeptide used in cellular expansion,  
PT immune response stimulation or treatment of pathological conditions  
XX contains amino acid substitutions at positions 8, 84, 118 or 122 -  
XX  
PS Claim 4; Page 88-89; 90pp; English.  
XX  
CC The invention relates to novel soluble flt3 ligand (flt3-L) polypeptides  
CC which exhibits increased or decreased biological activity relative to  
CC the full length wild type (AAV69719) or mature (AAV69720) flt3-L  
CC polypeptides. This sequence represents an example of the novel flt-3  
CC ligands and comprises the Q122R mutant polypeptide. The flt3-L protein  
CC binds cell surface tyrosine kinase receptors and regulate growth and  
CC differentiation of hematopoietic progenitor cells. The flt3-L protein can  
CC be used to induce cellular expansion (especially in vivo) or  
CC differentiation, e.g. in hematopoietic, natural killer (NK) or dendritic  
CC cells, especially in the presence of growth factors such as interleukins,  
CC colony stimulating factors or protein kinases. The protein can also  
CC modulate, augment or enhance a patient's immune response and can be used  
CC to treat an immune disorder (e.g. allergy, autoimmunity or  
CC immunosuppression). The protein may be used to treat a pathological  
CC condition e.g. myelodysplasia, aplastic anemia, HIV infection, breast,  
CC small cell lung, testicular or ovarian cancer, lymphoma, multiple  
CC myeloma, neuroblastoma or acute leukemia.  
XX  
XX Sequence 209 AA;  
SQ

Query Match 89.4%; Score 1110; DB 21; Length 209;  
Best Local Similarity 99.5%; Pred. No. 8.5e-97;









GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: April 1, 2002, 06:13:54 ; Search time 64.79 Seconds  
(without alignments)  
81.622 Million cell updates/sec

Title: US-08-162-407-6  
Perfect score: 1242  
Sequence: 1 MVLAPAMSPPTLYLLLL...RPEGVPPVSPQDLLVEH 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PCrUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1242	100.0	235	1 US-08-243-545-6	Sequence 6, Appli
2	1242	100.0	235	2 US-08-993-962-6	Sequence 6, Appli
3	1242	100.0	235	4 US-09-160-841-6	Sequence 6, Appli
4	1242	100.0	235	4 US-09-109-100-1	Sequence 1, Appli
5	1242	100.0	235	5 PCT-US94-05365-6	Sequence 6, Appli
6	1124	90.5	212	4 US-09-109-100-10	Sequence 10, Appli
7	1114	89.7	209	4 US-09-109-100-18	Sequence 18, Appli
8	1110	89.4	209	4 US-09-109-100-9	Sequence 9, Appli
9	1110	89.4	209	4 US-09-109-100-12	Sequence 12, Appli
10	1110	89.4	209	4 US-09-109-100-14	Sequence 14, Appli
11	1110	89.4	209	4 US-09-109-100-11	Sequence 11, Appli
12	1108	89.2	209	4 US-09-109-100-15	Sequence 15, Appli
13	1108	89.2	209	4 US-09-109-100-13	Sequence 13, Appli
14	1107	89.1	209	4 US-09-109-100-8	Sequence 8, Appli
15	1106	88.6	209	4 US-09-109-100-16	Sequence 16, Appli
16	1100	88.6	231	1 US-08-243-545-2	Sequence 2, Appli
17	768.5	61.9	231	2 US-08-993-962-2	Sequence 2, Appli
18	768.5	61.9	231	4 US-09-160-841-2	Sequence 2, Appli
19	768.5	61.9	231	5 PCT-US94-05365-2	Sequence 2, Appli
20	765.5	61.6	231	1 US-08-220-379B-7	Sequence 7, Appli
21	765.5	61.6	231	5 PCT-US95-03866-6	Sequence 6, Appli
22	506.5	40.8	137	4 US-09-109-100-19	Sequence 19, Appli
23	154	12.4	42	5 PCT-US94-05150-17	Sequence 17, Appli
24	91.5	7.4	675	1 US-08-317-522A-9	Sequence 9, Appli
25	91.5	7.4	675	1 US-08-439-818A-9	Sequence 9, Appli
26	91.5	7.4	675	1 US-08-751-965-9	Sequence 9, Appli
27	91.5	7.4	675	2 US-08-751-965-9	Sequence 9, Appli

28	91.5	7.4	675	2 US-08-738-975-9	Sequence 9, Appli
29	91.5	7.4	675	2 US-08-728-626-9	Sequence 9, Appli
30	91.5	7.4	675	3 US-08-808-599A-9	Sequence 9, Appli
31	87.5	7.0	415	4 US-09-006-353A-6	Sequence 6, Appli
32	85	6.8	366	1 US-08-004-492-8	Sequence 8, Appli
33	84.5	6.8	913	3 US-08-445-640-4	Sequence 4, Appli
34	84.5	6.8	913	3 US-08-170-558-4	Sequence 4, Appli
35	84.5	6.8	913	3 US-08-447-314-4	Sequence 4, Appli
36	84.5	6.8	913	3 US-08-445-461-4	Sequence 4, Appli
37	84	6.8	107	4 US-09-220-528-52	Sequence 52, Appli
38	84	6.8	220	4 US-09-220-528-26	Sequence 26, Appli
39	83.5	6.7	429	1 PCT-US94-589-2	Sequence 2, Appli
40	83.5	6.7	429	5 PCT-US93-02024-2	Sequence 2, Appli
41	83.5	6.7	671	3 US-09-121-321-16	Sequence 16, Appli
42	83.5	6.7	671	4 US-08-933-803A-16	Sequence 16, Appli
43	83	6.7	28	5 PCT-US94-05150-12	Sequence 12, Appli
44	83	6.7	758	1 US-07-756-250-16	Sequence 16, Appli
45	82.5	6.6	249	2 US-08-632-514C-11	Sequence 11, Appli

## ALIGNMENTS

RESULT 1  
US-08-243-545-6  
: Sequence 6, Application US/08243545  
: Patent No. 5554512  
: GENERAL INFORMATION:  
: APPLICANT: Lyman, Stewart D.  
: APPLICANT: Beckmann, M. Patricia  
: TITLE OF INVENTION: Ligands for f1c3/flk-2 Receptors  
: NUMBER OF SEQUENCES: 8  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
: STREET: 51 University Street  
: CITY: Seattle  
: STATE: Washington  
: COUNTRY: US  
: ZIP: 98101  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: Apple Macintosh  
: OPERATING SYSTEM: Macintosh 7.0.1  
: SOFTWARE: Microsoft Word, Version #5.1  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/243,545  
: FILING DATE: 11-MAY-1994  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/162,407  
: FILING DATE: 03-DEC-1993  
: APPLICATION NUMBER: 08/111,758  
: FILING DATE: August 25, 1993  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/106,463  
: FILING DATE: August 12, 1993  
: CLASSIFICATION: 435  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: 08/068,394  
: FILING DATE: May 24, 1993  
: CLASSIFICATION: 435  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Malaska, Stephen L.  
: REGISTRATION NUMBER: 32,655  
: REFERENCE/DOCKET NUMBER: 2813-C  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (206) 587-0430  
: TELEFAX: (206) 233-0644  
: TELEX: 755822  
: INFORMATION FOR SEQ ID NO: 6:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 235 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-243-545-6

Query Match 100.0%; Score 1242; DB 1; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1,4e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVLAPAWSPPTTLLLLLSGLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPVTV 60  
DB 1 MYVLAPAWSPPTTLLLLLSGLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPVTV 60  
QY 61 ASNLQDEELCGGLMRVLVLAORMMERLKTAVAGSKMOGLLEVRNTEIHVTKCAFQPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVLAORMMERLKTAVAGSKMOGLLEVRNTEIHVTKCAFQPPSCL 120  
QY 121 RFVQNTISRLOETSEQLVAKPWITRQNSRCLQLQCPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQNTISRLOETSEQLVAKPWITRQNSRCLQLQCPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPPLLLLLLPVGLLLAAACLIHQRTRRTPRPGQVPPVPSQDILLVEH 235  
DB 181 APQPPLLLLLLPVGLLLAAACLIHQRTRRTPRPGQVPPVPSQDILLVEH 235

## RESULT 2

US-08-993-962-6  
Sequence 6, Application US/08993962  
Patent No. 5843423

## GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,962  
FILING DATE: December 18, 1997

## CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993

## CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993

## CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644

TELEX: 756922  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 235 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-993-962-6

Query Match 100.0%; Score 1242; DB 2; Length 235;  
Best Local Similarity 100.0%; Pred. No. 1,4e-117;  
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MYVLAPAWSPPTTLLLLLSGLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPVTV 60  
DB 1 MYVLAPAWSPPTTLLLLLSGLSGTQDCSFQHSPISSDPAVKIRLSYLLQDYPVTV 60  
QY 61 ASNLQDEELCGGLMRVLVLAORMMERLKTAVAGSKMOGLLEVRNTEIHVTKCAFQPPSCL 120  
DB 61 ASNLQDEELCGGLMRVLVLAORMMERLKTAVAGSKMOGLLEVRNTEIHVTKCAFQPPSCL 120  
QY 121 RFVQNTISRLOETSEQLVAKPWITRQNSRCLQLQCPDSSSTLPPWSPRPLEATAPT 180  
DB 121 RFVQNTISRLOETSEQLVAKPWITRQNSRCLQLQCPDSSSTLPPWSPRPLEATAPT 180  
QY 181 APQPPLLLLLLPVGLLLAAACLIHQRTRRTPRPGQVPPVPSQDILLVEH 235  
DB 181 APQPPLLLLLLPVGLLLAAACLIHQRTRRTPRPGQVPPVPSQDILLVEH 235

## RESULT 3

US-09-160-841-6  
Sequence 6, Application US/09160841  
Patent No. 6190655

## GENERAL INFORMATION:

APPLICANT: Lyman, Stewart D.  
APPLICANT: Beckmann, M. Patricia  
TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Stephen L. Malaska, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0.1  
SOFTWARE: Microsoft Word, Version #5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/160,841  
FILING DATE:

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/162,407  
FILING DATE: December 3, 1993  
APPLICATION NUMBER: 08/111,758  
FILING DATE: August 25, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/106,463  
FILING DATE: August 12, 1993

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/068,394  
FILING DATE: May 24, 1993

## CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Malaska, Stephen L.  
REGISTRATION NUMBER: 32,655  
REFERENCE/DOCKET NUMBER: 2813-C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644





;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 12  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-12

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 2.4e-104;  
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 27 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 86  
DB 1 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 60  
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DB 121 R0NFSRCL0COPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLPVGLLLAAACMH 180  
OY 207 W0TRRRRTPRPGE0VPPVPSPODLLVEH 235  
DB 181 W0TRRRRTPRPGE0VPPVPSPODLLVEH 209

RESULT 10  
US-09-109-100-14  
;; Sequence 14, Application US/09109100C  
;; Patent No. 6291661  
;; GENERAL INFORMATION:  
;; APPLICANT: Graddis, Thomas J.  
;; APPLICANT: McGrew, Jeffrey T.  
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
;; FILE REFERENCE: 03260.0028  
;; CURRENT APPLICATION NUMBER: US/09/109,100C  
;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 14  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-14

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 2.4e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 86  
DB 1 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVOTNISRLLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVOTNISRLLQETSEQVALKPWIT 120  
OY 147 R0NFSRCL0COPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLPVGLLLAAACMH 206  
DB 121 R0NFSRCL0COPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLPVGLLLAAACMH 180  
OY 207 W0TRRRRTPRPGE0VPPVPSPODLLVEH 235  
DB 181 W0TRRRRTPRPGE0VPPVPSPODLLVEH 209

RESULT 11

US-09-109-100-17  
;; Sequence 17, Application US/09109100C  
;; Patent No. 6291661  
;; GENERAL INFORMATION:  
;; APPLICANT: Graddis, Thomas J.  
;; APPLICANT: McGrew, Jeffrey T.  
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
;; FILE REFERENCE: 03260.0028  
;; CURRENT APPLICATION NUMBER: US/09/109,100C  
;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 17  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-17

Query Match 89.4%; Score 1110; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 2.4e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 86  
DB 1 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVOTNISRLLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVOTNISRLLQETSEQVALKPWIT 120  
OY 147 R0NFSRCL0COPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLPVGLLLAAACMH 206  
DB 121 R0NFSRCL0COPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLPVGLLLAAACMH 180  
OY 207 W0TRRRRTPRPGE0VPPVPSPODLLVEH 235  
DB 181 W0TRRRRTPRPGE0VPPVPSPODLLVEH 209

RESULT 12  
US-09-109-100-11  
;; Sequence 11, Application US/09109100C  
;; Patent No. 6291661  
;; GENERAL INFORMATION:  
;; APPLICANT: Graddis, Thomas J.  
;; APPLICANT: McGrew, Jeffrey T.  
;; TITLE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE  
;; FILE REFERENCE: 03260.0028  
;; CURRENT APPLICATION NUMBER: US/09/109,100C  
;; CURRENT FILING DATE: 1998-07-02  
;; NUMBER OF SEQ ID NOS: 20  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 11  
;; LENGTH: 209  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-109-100-11

Query Match 89.2%; Score 1108; DB 4; Length 209;  
Best Local Similarity 99.5%; Pred. No. 3.8e-104;  
Matches 208; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 27 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 86  
DB 1 TODCSFOHSPISSDFAVKIRELSDYLLDYPYTVASNL0DEELCGMLRVLAORMERL 60  
OY 87 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVOTNISRLLQETSEQVALKPWIT 146  
DB 61 KTVAGSKMOGLLEERVNTEIHFTKCAFOPPPSCLRFVOTNISRLLQETSEQVALKPWIT 120  
OY 147 R0NFSRCL0COPDSSSTLPPWSPRPLEATAPTAPOPPLLLLLPVGLLLAAACMH 206

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Db 121 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180
QY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 13
US-09-109-100-15
; Sequence 15, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; FILE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-15

Query Match 89.2%; Score 1108; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 3.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMMERL 86
Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMMERL 60

QY 87 KTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
Db 61 KTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 206
Db 121 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 14
US-09-109-100-13
; Sequence 13, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; FILE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-13

Query Match 89.1%; Score 1107; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 4.8e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 27 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMMERL 86
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QY 87 KTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
Db 61 KTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 206
Db 121 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209

RESULT 15
US-09-109-100-8
; Sequence 8, Application US/09109100C
; Patent No. 6291661
; GENERAL INFORMATION:
; APPLICANT: Graddis, Thomas J.
; APPLICANT: McGrew, Jeffrey T.
; FILE OF INVENTION: FLT3-L MUTANTS AND METHODS OF USE
; FILE REFERENCE: 03260.0028
; CURRENT APPLICATION NUMBER: US/09/109,100C
; CURRENT FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-109-100-8

Query Match 89.0%; Score 1106; DB 4; Length 209;
Best Local Similarity 99.5%; Pred. No. 6.1e-104;
Matches 208; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 TQDCSFQHSPISSDFAVKIRELSYLLQDYPVTVASNLQDEELCGGLMRVLVAQRMMERL 60

QY 87 KTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 146
Db 61 KTVAGSKMGGLLEVRNTEIHVTKCAFQPPSCLEFVQTNISRLQETSEQLVALKPMIT 120

QY 147 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 206
Db 121 RQNFSCLELQCCOPDSSSTLPPMSPRPLEATAPAPQPLLLLLLLPVGLLLAAACLH 180

QY 207 WQTRRRTPRPGEOVPPVPSPODLLVEH 235
Db 181 WQTRRRTPRPGEOVPPVPSPODLLVEH 209
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Mon Apr 1 06:15:15 2002

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